GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 09:50:25 ; Search time 46 Seconds
(without alignments)
744.081 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 2130
Sequence: 1 MNPTLGLAIFLAVLLTVKGL.....YSEKIPSVLFLGKIVNPIGK 414

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2130	100.0	414	2	US-09-755-665-14	Sequence 14, Appl
2	2130	100.0	414	2	US-09-755-665-55	Sequence 55, Appl
3	2130	100.0	414	2	US-09-755-665-56	Sequence 56, Appl
4	2130	100.0	415	2	US-09-461-325-134	Sequence 134, App
5	2130	100.0	415	2	US-10-012-542-134	Sequence 134, App
6	2130	100.0	415	2	US-10-115-123-134	Sequence 134, App
7	1798	84.4	361	2	US-09-755-665-57	Sequence 57, Appl
8	842	39.5	377	2	US-10-037-417-66	Sequence 66, Appl
9	798	37.5	394	2	US-08-481-534-6	Sequence 6, Appli
10	792	37.2	394	2	US-08-481-534-11	Sequence 11, Appl
11	791	37.1	394	2	US-08-481-534-9	Sequence 9, Appli
12	790	37.1	394	1	US-08-002-202-6	Sequence 6, Appli
13	790	37.1	394	1	US-08-553-488A-1	Sequence 1, Appli
14	785	36.9	363	2	US-09-755-665-58	Sequence 58, Appl
15	785	36.9	394	2	US-09-023-339-1	Sequence 1, Appli
16	785	36.9	418	1	US-08-121-714-3	Sequence 3, Appli
17	785	36.9	418	1	US-08-477-108A-3	Sequence 3, Appli
18	785	36.9	418	1	US-08-477-112-3	Sequence 3, Appli
19	785	36.9	418	2	US-10-030-330-3	Sequence 3, Appli
20	785	36.9	418	4	PCT-US93-08322-3	Sequence 3, Appli
21	784	36.8	394	1	US-08-002-202-11	Sequence 11, Appl
22	783	36.8	394	1	US-08-002-202-9	Sequence 9, Appli
23	780	36.6	418	2	US-10-000-489-92	Sequence 92, Appl
24	776	36.4	414	2	US-09-518-098B-19	Sequence 19, Appl
25	772.5	36.3	360	2	US-10-037-417-67	Sequence 67, Appl
26	772	36.2	414	1	US-08-002-202-17	Sequence 17, Appl
27	772	36.2	414	2	US-08-481-534-17	Sequence 17, Appl
28	766	36.0	414	1	US-08-002-202-13	Sequence 13, Appl
29	766	36.0	414	2	US-08-481-534-13	Sequence 13, Appl
30	765	35.9	414	1	US-08-002-202-19	Sequence 19, Appl
31	765	35.9	414	2	US-08-481-534-19	Sequence 19, Appl
32	725.5	34.1	414	2	US-09-949-016-8143	Sequence 8143, Ap
33	709.5	33.3	351	2	US-10-000-489-50	Sequence 50, Appl
34	706	33.1	448	2	US-10-104-047-3380	Sequence 3380, Ap
35	703.5	33.0	423	2	US-09-976-594-19	Sequence 19, Appl
36	703.5	33.0	423	2	US-09-919-039-19	Sequence 19, Appl
37	703.5	33.0	435	2	US-09-912-628-5	Sequence 5, Appli
38	701.5	32.9	415	2	US-09-919-039-390	Sequence 390, App
39	698.5	32.8	419	2	US-09-949-016-11541	Sequence 11541, A
40	698	32.8	422	2	US-09-244-111-8	Sequence 8, Appli
41	690.5	32.4	417	2	US-10-012-231A-236	Sequence 236, App
42	690.5	32.4	417	2	US-10-015-389A-236	Sequence 236, App
43	690.5	32.4	417	2	US-10-006-768A-236	Sequence 236, App
44	690.5	32.4	417	2	US-10-015-671A-236	Sequence 236, App
45	690.5	32.4	417	2	US-10-015-393A-236	Sequence 236, App

ALIGNMENTS

RESULT 1
US-09-755-665-14
; Sequence 14, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Taillon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-14

Query Match 100.0%; Score 2130; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.7e-197;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
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Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 2
US-09-755-665-55
; Sequence 55, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
;  APPLICANT: Prayaga, Sudhirdas K.
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Taillon, Bruce E.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  MacDougall, John
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-631
;  CURRENT APPLICATION NUMBER: US/09/755,665
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
;   LENGTH: 414
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-755-665-55

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  Best Local Similarity  100.0%;  Pred. No. 1.7e-197;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 3
US-09-755-665-56
; Sequence 56, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
;  APPLICANT: Prayaga, Sudhirdas K.
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Taillon, Bruce E.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  MacDougall, John
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-631
;  CURRENT APPLICATION NUMBER: US/09/755,665
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
;   LENGTH: 414
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-755-665-56

  Query Match           100.0%;  Score 2130;  DB 2;  Length 414;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-197;
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Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
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RESULT 4
US-09-461-325-134
; Sequence 134, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029P1
;  CURRENT APPLICATION NUMBER: US/09/461,325A
;  CURRENT FILING DATE: 1999-12-14
;  EARLIER APPLICATION NUMBER: PCT/US99/13418
;  EARLIER FILING DATE: 1999-06-15
;  EARLIER APPLICATION NUMBER: 60/089,507
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/089,508
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/089,509
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/089,510
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/090,112
;  EARLIER FILING DATE: 1998-06-22
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;  EARLIER APPLICATION NUMBER: 60/090,113
;  EARLIER FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
;   LENGTH: 415
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (415)
;   OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring L-amino acids
US-09-461-325-134

  Query Match           100.0%;  Score 2130;  DB 2;  Length 415;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-197;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
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Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
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Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
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Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
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Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 5
US-10-012-542-134
; Sequence 134, Application US/10012542
; Patent No. 6627741
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029P1
;  CURRENT APPLICATION NUMBER: US/10/012,542
;  CURRENT FILING DATE:  2001-12-12
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
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;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
;   LENGTH: 415
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (415)
;   OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring L-amino
;   OTHER INFORMATION: acids
US-10-012-542-134

  Query Match           100.0%;  Score 2130;  DB 2;  Length 415;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-197;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 6
US-10-115-123-134
; Sequence 134, Application US/10115123
; Patent No. 6774216
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029G30AP1D2
;  CURRENT APPLICATION NUMBER: US/10/115,123
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: PCT/US99/13418
;  PRIOR FILING DATE: 1999-06-15
;  PRIOR APPLICATION NUMBER: 60/089,507
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,508
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,509
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,510
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/090,112
;  PRIOR FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: 60/090,113
;  PRIOR FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
;   LENGTH: 415
;   TYPE: PRT
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;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (415)
;   OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring L-amino acids
US-10-115-123-134

  Query Match           100.0%;  Score 2130;  DB 2;  Length 415;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-197;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 7
US-09-755-665-57
; Sequence 57, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
;  APPLICANT: Prayaga, Sudhirdas K.
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Taillon, Bruce E.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  MacDougall, John
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-631
;  CURRENT APPLICATION NUMBER: US/09/755,665
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
;   LENGTH: 361
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)..(361)
;   OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
;   OTHER INFORMATION: specification
US-09-755-665-57

  Query Match           84.4%;  Score 1798;  DB 2;  Length 361;
  Best Local Similarity  96.7%;  Pred. No. 1.9e-165;
  Matches  349;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLH 113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLH 60

Qy        114 EGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMA 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMA 120

Qy        174 QKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKN 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKN 180

Qy        234 SSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFS 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFS 240

Qy        294 RWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 RWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 300

Qy        354 HKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIG 413
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 HKAELKMDERXXXXXXXXXXXXLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIG 360

Qy        414 K 414
              |
Db        361 K 361


RESULT 8
US-10-037-417-66
; Sequence 66, Application US/10037417
; Patent No. 6903201
; GENERAL INFORMATION:
;  APPLICANT: Kekuda, Ramesh
;  APPLICANT:  Alsobrook II, John P
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Lepley, Denise M
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Vernet, Corine A.M.
;  APPLICANT:  Li, Li
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Edinger, Shlomit R
;  APPLICANT:  Sciore, Paul
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Rothenberg, Mark
;  APPLICANT:  Stone, David J
;  APPLICANT:  Boldog, Ferenc L
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Anderson, David W
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Miller, Charles E
;  APPLICANT:  Eisen, Andrew J
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-235
;  CURRENT APPLICATION NUMBER: US/10/037,417
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: 60/260,018
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: 60/260,360
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/272,411
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: 60/272,817
;  PRIOR FILING DATE: 2001-03-02
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;  PRIOR APPLICATION NUMBER: 60/291,186
;  PRIOR FILING DATE: 2001-05-15
;  PRIOR APPLICATION NUMBER: 60/303,231
;  PRIOR FILING DATE: 2001-07-05
;  PRIOR APPLICATION NUMBER: 60/305,060
;  PRIOR FILING DATE: 2001-07-12
;  PRIOR APPLICATION NUMBER: 60/318,405
;  PRIOR FILING DATE: 2001-09-10
;  PRIOR APPLICATION NUMBER: 60/318,700
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
;   LENGTH: 377
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Serpin
;   OTHER INFORMATION: Consensus Sequence
US-10-037-417-66

  Query Match             39.5%;  Score 842;  DB 2;  Length 377;
  Best Local Similarity   43.7%;  Pred. No. 6.6e-73;
  Matches  163;  Conservative   86;  Mismatches  118;  Indels    6;  Gaps    4;

Qy         45 AKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQ--GF 102
              | :||  | |  | | |:|   || :||| ||:|||:| :|| |||: :|  :| :  ||
Db          5 ALKLASANADFAFSLYKELVEQNPDKNIFFSPVSISSALAMLSLGAKGNTATQILEVLGF 64

Qy        103 NFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAET 162
              |  :  | ::|:|| ::: || :    |:|: || ||:|: |:   :||||:|  | :|
Db         65 NLTETSEAEIHQGFQHLLQELNRPDTGLQLTTGNALFVDKSLKLLDEFLEDSKRLYQSEV 124

Qy        163 ILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNV 222
              :| : | |:|||||:: :|| ||| :|::::|  ||::| |||:|: :||  ||| :
Db        125 FSVDFSDPEEAKKQINDWVEKKTQGKIKDLLKDLDSDTVLVLVNYIYFKGKWKKPFDPEL 184

Qy        223 TKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITA-IFILPDE-GKL 280
              |:|||| ::| ::|||||| : | :     |::|:| :||:||: | |: :|||||| |||
Db        185 TEEEDFHVDKKTTVKVPMMNQLGTFYYFRDEELNCKVLELPYKGNATSMLFILPDEVGKL 244

Qy        281 KHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTK 340
              : :|  |  :|  :|  :  | |:: :|:  : ||:|||  |: :|:: :|    ||:
Db        245 EQVEAALSPETLRKWLENMEPREVELYLPKFSIEGTYDLKDVLAKLGITDLFSNQADLSG 304

Qy        341 IAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPMETP--LVVKIDKPYLLLIYSEK 398
              |:    ||| :||||| |::|| ||| || |||  :|   |  |    |:|:| ||| :
Db        305 ISEDEDLKVSKAVHKAVLEVDEEGTEAAAATGAIIVPRSLPPELEFTADRPFLFLIYDDP 364

Qy        399 IPSVLFLGKIVNP 411
               |:||:||:|||
Db        365 TGSILFMGKVVNP 377


RESULT 9
US-08-481-534-6
; Sequence 6, Application US/08481534
; Patent No. 6022855
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Gary
;    APPLICANT:  Anderson, Eric D
;    APPLICANT:  Thomas, Laurel
;    APPLICANT:  Hayflick, Joel S
;    APPLICANT:  Nelson, Jay
;    APPLICANT:  Stenglen, Stephan G
;    TITLE OF INVENTION:  Methods and Reagents for Inhibiting Furin
;    TITLE OF INVENTION:  Endoprotease
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDonnell Boehnen Hulbert & Berghoff
;      STREET:  300 South Wacker Drive
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/481,534
;      FILING DATE:  14-SEP-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6022855nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  92,448-D
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-913-0001
;      TELEFAX:  312-913-0002
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  394 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-481-534-6

  Query Match             37.5%;  Score 798;  DB 2;  Length 394;
  Best Local Similarity   43.3%;  Pred. No. 1.3e-68;
  Matches  157;  Conservative   72;  Mismatches  132;  Indels    2;  Gaps    1;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
              :  | | ::||  :   ||| ||:||:|||:|| || :  | ||| :| ||   ::||
Db         32 EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTQIPEAQ 91

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
              :||||  ::  | |    |:|: || ||: | |:   ||||| |  | :|    || : |
Db         92 IHEGFQELLRTLNQPDSQLQLTTGNGLFLSQGLKLVDKFLEDVKKLYHSEAFTVNFGDTE 151

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
              |:|||||:: : | ||| :|:: :|  ||  | |||||: :|:  |:   |:|||| ::
Db        152 QAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVD 211

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
              : ::|||||| | |:: : :  |||  :| : |  | |||| |||||||:|||  |  |
Db        212 QVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 271

Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
               :::     ||   : :|:| :|||:|||  |  :|::|:|    ||: :     ||: :
Db        272 ITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSK 331

Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              ||||| | :||:||| |     : :||  |  || :||:: |:  :   | ||:||:|||
Db        332 AVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNP 391

Qy        412 IGK 414
               ||
Db        392 TGK 394


RESULT 10
US-08-481-534-11
; Sequence 11, Application US/08481534
; Patent No. 6022855
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Gary
;    APPLICANT:  Anderson, Eric D
;    APPLICANT:  Thomas, Laurel
;    APPLICANT:  Hayflick, Joel S
;    APPLICANT:  Nelson, Jay
;    APPLICANT:  Stenglen, Stephan G
;    TITLE OF INVENTION:  Methods and Reagents for Inhibiting Furin
;    TITLE OF INVENTION:  Endoprotease
```

```
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDonnell Boehnen Hulbert & Berghoff
;      STREET:  300 South Wacker Drive
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/481,534
;      FILING DATE:  14-SEP-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6022855nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  92,448-D
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-913-0001
;      TELEFAX:  312-913-0002
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  394 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Modified site
;      LOCATION:  355..358
;      OTHER INFORMATION:  /label=Variant
;      OTHER INFORMATION:  / note="The amino acid sequence is the amino acid
;      OTHER INFORMATION:  sequence of the modified alpha-1-antitrypsin
;      OTHER INFORMATION:  protein, alpha-1-antitrypsin Pittsburgh."
US-08-481-534-11

  Query Match             37.2%;  Score 792;  DB 2;  Length 394;
  Best Local Similarity   43.0%;  Pred. No. 4.8e-68;
  Matches  156;  Conservative   72;  Mismatches  133;  Indels    2;  Gaps    1;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
              :  | | ::||  :   ||| ||:||:|||:|| || :  | ||| :| ||   ::||
Db         32 EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTQIPEAQ 91

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
              :|||| ::  | |    |:|: || ||: | |:   ||||| |  | :|    || : |
Db         92 IHEGFQELLRTLNQPDSQLQLTTGNGLFLSQGLKLVDKFLEDVKKLYHSEAFTVNFGDTE 151

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
              |:|||||:: : | ||| :|:: :|  ||  | |||||: :|:  |:   |:|||| ::
Db        152 QAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVD 211

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
              : ::|||||| | |:: : :  |||  :| : |  | |||| |||||||:|||  |  |
Db        212 QVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 271

Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
              :::      ||   : :|:| :|||:||| |  :|::|:|    ||: :    ||: :
Db        272 ITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSK 331

Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              ||||| | :||:||| |     : :|   |  || :||:: |:  :   | ||:||:|||
Db        332 AVHKAVLTIDEKGTEAAGAMFLEAIPRSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNP 391

Qy        412 IGK 414
              ||
Db        392 TGK 394
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RESULT 11
US-08-481-534-9
; Sequence 9, Application US/08481534
; Patent No. 6022855
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Gary
;    APPLICANT:  Anderson, Eric D
;    APPLICANT:  Thomas, Laurel
;    APPLICANT:  Hayflick, Joel S
;    APPLICANT:  Nelson, Jay
;    APPLICANT:  Stenglen, Stephan G
;    TITLE OF INVENTION:  Methods and Reagents for Inhibiting Furin
;    TITLE OF INVENTION:  Endoprotease
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDonnell Boehnen Hulbert & Berghoff
;      STREET:  300 South Wacker Drive
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/481,534
;      FILING DATE:  14-SEP-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6022855nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  92,448-D
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-913-0001
;      TELEFAX:  312-913-0002
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  394 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Modified site
;      LOCATION:  355..358
;      OTHER INFORMATION:  /label=Variant
;      OTHER INFORMATION:  / note="The amino acid sequence is the amino acid
;      OTHER INFORMATION:  sequence of the modified alpha-1-antitrypsin
;      OTHER INFORMATION:  protein, alpha-1-antitrypsin Portland."
US-08-481-534-9

  Query Match             37.1%;  Score 791;  DB 2;  Length 394;
  Best Local Similarity   43.0%;  Pred. No. 6e-68;
  Matches  156;  Conservative   72;  Mismatches  133;  Indels    2;  Gaps    1;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
              :  | | ::||  :   ||| ||:||:|||:|| || :  | ||| :| ||   ::||
Db         32 EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTQIPEAQ 91

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
              :|||| ::  | |    |:|: || ||: | |:   ||||| |  | :|    || : |
Db         92 IHEGFQELLRTLNQPDSQLQLTTGNGLFLSQGLKLVDKFLEDVKKLYHSEAFTVNFGDTE 151

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
              |:|||||:: : | ||| :|:: :|  ||  | |||||: :|:  |:   |:|||| ::
Db        152 QAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVD 211

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
              : ::|||||| | |:: : :  |||  :| : |  | |||| |||||||:|||  |  |
Db        212 QVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 271
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Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
              :::     ||   : :|:| :|||:||| | :|::|:|    ||: :     ||: :
Db        272 ITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSK 331

Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              ||||| | :||:||| |     : :|   |  || :||:: |:  :   | ||:||:|||
Db        332 AVHKAVLTIDEKGTEAAGAMFLERIPRSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNP 391

Qy        412 IGK 414
              ||
Db        392 TGK 394


RESULT 12
US-08-002-202-6
; Sequence 6, Application US/08002202
; Patent No. 5604201
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Garry
;    APPLICANT:  Anderson, Eric D
;    APPLICANT:  Thomas, Laurel
;    APPLICANT:  Hayflick, Joel S
;    TITLE OF INVENTION:  Methods and Reagents for Inhibiting
;    TITLE OF INVENTION:  Purin Endoprotease
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Allegretti and Witcoff, Ltd.
;      STREET:  10 South Wacker Drive, Suite 3000
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/002,202
;      FILING DATE:  08-JAN-1993
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5604201nan, Kevin E
;      REGISTRATION NUMBER:  35,30003
;      REFERENCE/DOCKET NUMBER:  92,448
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;      TELEX:  910-221-5317
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  394 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-002-202-6

  Query Match           37.1%;  Score 790;  DB 1;  Length 394;
  Best Local Similarity   43.0%;  Pred. No. 7.5e-68;
  Matches  156;  Conservative   72;  Mismatches  133;  Indels    2;  Gaps    1;

Qy         54 DLGPKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
              :  | | ::||  :   ||| ||:||:|||:|| || :  | ||| :| ||   ::||
Db         32 EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQ 91

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
              :|||| ::  | |    |:|: || ||: | |:   ||||| |  | :|    || : |
Db         92 IHEGFQELLRTLNQPDSQLQLTTGNGLFLSQGLKLVDKFLEDVKKLYHSEAFTVNFGDTE 151

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
              |:|||||:: : | ||| :|:: :|  ||  | |||||: :|:  |:   |:|||| ::
Db        152 QAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVD 211

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
              : ::|||||| | |:: : :  |||  :| : |  | |||| |||||||:|||  | |
Db        212 QVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 271

Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
              :::     ||   : :|:| :|||:|||  | :|::|:|    ||: :     ||: :
Db        272 ITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSK 331

Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              ||||| | :||:||| |     : :||  |  || :||:: |:  :   | ||:||:|||
Db        332 AVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNP 391

Qy        412 IGK 414
              |
Db        392 TQK 394


RESULT 13
US-08-553-488A-1
; Sequence 1, Application US/08553488A
; Patent No. 5817484
;  GENERAL INFORMATION:
;    APPLICANT:  YU, Myeong-Hee
;    APPLICANT:  KWON, Ki-Sun
;    APPLICANT:  LEE, Kee-Nyung
;    APPLICANT:  SHIN, Hwa-Soo
;    TITLE OF INVENTION:  THERMORESISTANT ALPHA-1-ANTITRYPSIN
;    TITLE OF INVENTION:  MUTEIN
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  YU, Myeong-Hee
;      STREET:  3-1003, Hankang Apartment, 49-8, Jamwon-dong,
;      STREET:  Seocho-gu
;      CITY:  Seoul
;      STATE:  Seoul
;      COUNTRY:  Republic of Korea
;      ZIP:  137-030
;      ADDRESSEE:  KWON, Ki-Sun
;      STREET:  130-1306, Hanbit Apartment, Oun-dong,
;      STREET:  Yuseong-gu
;      CITY:  Taejon
;      STATE:  Taejon
;      COUNTRY:  Republic of Korea
;      ZIP:  305-333
;      ADDRESSEE:  LEE, Kee-Nyung
;      STREET:  105-1004, Hanbit Apartment, Oun-dong,
;      STREET:  Yuseong-gu
;      CITY:  Taejon
;      STATE:  Taejon
;      COUNTRY:  Republic of Korea
;      ZIP:  305-333
;      ADDRESSEE:  SHIN, Hwa-Soo
;      STREET:  3-303, Sindonga Apartment, Yongjeon-dong,
;      STREET:  Dong-gu
;      CITY:  Taejon
;      STATE:  Taejon
;      COUNTRY:  Republic of Korea
;      ZIP:  300-200
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5inch, 1.44MB storage
;      COMPUTER:  IBM PC/AT
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/553,488A
;      FILING DATE:  20-NOV-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  KR 93-8510
;      FILING DATE:  18-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:
;      REGISTRATION NUMBER:
```

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;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:
;      TELEFAX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  394 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      OTHER INFORMATION:  wild type human '-1-antitrypsin
US-08-553-488A-1

  Query Match           37.1%;  Score 790;  DB 1;  Length 394;
  Best Local Similarity   42.7%;  Pred. No. 7.5e-68;
  Matches  155;  Conservative   74;  Mismatches  132;  Indels    2;  Gaps    1;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
              :  | | ::||  :   ||| ||:||:|||:|| :| :  | ||| :| ||   ::||
Db         32 EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSVGTKADTHDEILEGLNFNLTEIPEAQ 91

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
              :|||  ::| | |    |:|: || ||: : |:   |||| |  | :|    || : |
Db         92 IHEGFQELLHTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTE 151

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
              |:|||::: : | ||| :|:: :|  ||  | |||||: :|:  |:   |:|||| ::
Db        152 EAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVD 211

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
              : ::|||||| | |:: : :  ||| :| : |  | |||| |||||||:|||  |  |
Db        212 QVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 271

Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
               :::     ||   : :|:| :|||:|||  |  :|::|:|    ||: :     ||: :
Db        272 ITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSK 331

Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              ||||| | :||:||| |     : :||  |  || :||:: |:  :   | ||:||:|||
Db        332 AVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIDQNTKSPLFMGKVVNP 391

Qy        412 IGK 414
                |
Db        392 TQK 394


RESULT 14
US-09-755-665-58
; Sequence 58, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
;  APPLICANT: Prayaga, Sudhirdas K.
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Taillon, Bruce E.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  MacDougall, John
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-631
;  CURRENT APPLICATION NUMBER: US/09/755,665
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
;   LENGTH: 363
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-755-665-58

  Query Match           36.9%;  Score 785;  DB 2;  Length 363;
  Best Local Similarity   41.6%;  Pred. No. 2e-67;
  Matches  151;  Conservative   83;  Mismatches  127;  Indels    2;  Gaps    1;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
              :  | | ::||  :   ||| ||:||:|||:|| :| :  | ||| :| ||   ::||:
Db          1 EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTQSEILEGLNFNLTEIPQAQ 60

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
              :|||  ::  | :    |:|: || ||::: |:   ||||| || | :|    |||: |
Db         61 VHEGFQELLRTLNKPDSQLQLTTGNGLFLNKSLKVVDKFLEDVKNLYHSEAFSVNFQDTE 120

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
              |:|||::: : | ||: :|:: :|  ||  | |||||: :|:  |:   |:|||| ::
Db        121 EAKKQINNYVEKGTQGKVVDLVKELDRDTVFALVNYIFFKGKWERPFEVEATEEEDFHVD 180

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
              : ::|||||| | |:: : :  ||| :| : |  | |||| |||||||:|||  |  |
Db        181 QATTVKVPMMRRLGMFNIYHCEKLSSWVLLMKYLGNATAIFFLPDQGKLQHLENELTHDI 240

Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
               :::     :||  :: :|:| :|||:|||  | ::|::|:|    ||: :     ||: :
Db        241 ITKFLENENRRSANLHLPKLAITGTYDLKTVLGHLGITKVFSNGADLSGVTEDAPLKLSK 300

Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              ||||| | :||:||| |     : :||  |  || :||:: |:  :   | ||:||:|||
Db        301 AVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFIGKVVNP 360

Qy        412 IGK 414
                |
Db        361 TQK 363


RESULT 15
US-09-023-339-1
; Sequence 1, Application US/09023339
; Patent No. 6127145
;  GENERAL INFORMATION:
;    APPLICANT:  Sutliff, Thomas D.
;    APPLICANT:  Rodriguez, Raymond L.
;    TITLE OF INVENTION:  Production of '1-Antitrypsin
;    TITLE OF INVENTION:  in Plants
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  P.O. Box 60850
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,339
;      FILING DATE:  13-FEB-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/037,991
;      FILING DATE:  13-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petithory, Joanne R
;      REGISTRATION NUMBER:  P42,995
;      REFERENCE/DOCKET NUMBER:  0665-0003.30
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-324-0880
;      TELEFAX:  650-324-0960
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  394 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
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; IMMEDIATE SOURCE:
; CLONE: mature AAT amino acid sequence
US-09-023-339-1

Query Match 36.9%; Score 785; DB 2; Length 394;
Best Local Similarity 42.7%; Pred. No. 2.3e-67;
Matches 155; Conservative 73; Mismatches 133; Indels 2; Gaps 1;

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Qy          54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
               :  | | ::||  :   ||| ||:||:|||:|| || :  | ||| :| ||   ::||
Db          32 EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQ 91

Qy         112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
               :|||| ::  | |    |:|: || ||: : |:   ||||| |  | :|    || : |
Db          92 IHEGFQELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTE 151

Qy         172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
                |:|||||:: : | ||| :|:: :|  ||  | |||||: :|:  |:   |:|||| ::
Db         152 EAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVD 211

Qy         232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
               : ::|||||| | |:: : :  |||  :| : |  | |||| |||||||:|||  |  |
Db         212 QVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 271

Qy         292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
                :::    ||   : :|:| :|||:|||  |  :|::|:|    ||: :     ||: :
Db         272 ITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSK 331

Qy         352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
               ||||| | :||:||| |     : :||  |  || :||:: |:  :   | ||:||:|||
Db         332 AVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNP 391

Qy         412 IGK 414
                |
Db         392 TQK 394
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Search completed: March 31, 2006, 09:51:43
Job time : 47 secs

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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 2
US-09-755-665-55
; Sequence 55, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
;  APPLICANT: Prayaga, Sudhirdas K.
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Taillon, Bruce E.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  MacDougall, John
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-631
;  CURRENT APPLICATION NUMBER: US/09/755,665
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
;   LENGTH: 414
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-755-665-55

  Query Match           100.0%;  Score 2130;  DB 2;  Length 414;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-197;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 3
US-09-755-665-56
; Sequence 56, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
;  APPLICANT: Prayaga, Sudhirdas K.
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Taillon, Bruce E.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  MacDougall, John
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-631
;  CURRENT APPLICATION NUMBER: US/09/755,665
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
;   LENGTH: 414
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-755-665-56

  Query Match           100.0%;  Score 2130;  DB 2;  Length 414;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-197;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 4
US-09-461-325-134
; Sequence 134, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029P1
;  CURRENT APPLICATION NUMBER: US/09/461,325A
;  CURRENT FILING DATE: 1999-12-14
;  EARLIER APPLICATION NUMBER: PCT/US99/13418
;  EARLIER FILING DATE: 1999-06-15
;  EARLIER APPLICATION NUMBER: 60/089,507
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/089,508
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/089,509
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/089,510
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/090,112
;  EARLIER FILING DATE: 1998-06-22
```

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 09:41:45 ; Search time 188 Seconds
(without alignments)
967.568 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 2130
Sequence: 1 MNPTLGLAIFLAVLLTVKGL.....YSEKIPSVLFLGKIVNPIGK 414

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
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4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2130	100.0	414	4	AAU05754	Aau05754 Human NOV
2	2130	100.0	414	4	AAE04885	Aae04885 Human pro
3	2130	100.0	414	6	ADA57300	Ada57300 Human sec
4	2130	100.0	414	6	ADA41179	Ada41179 Human sec
5	2130	100.0	414	8	ADN05952	Adn05952 Antipsori
6	2130	100.0	415	3	AAY86217	Aay86217 Human sec
7	2130	100.0	415	6	ABO53360	Abo53360 Novel hum
8	2123	99.7	414	4	AAM78898	Aam78898 Human pro
9	2114	99.2	431	4	ABB11832	Abb11832 Human sec
10	2114	99.2	431	4	AAM79882	Aam79882 Human pro
11	1783	83.7	358	4	AAU05759	Aau05759 Human NOV
12	795	37.3	418	1	AAP50877	Aap50877 Sequence
13	792	37.2	394	2	AAY44205	Aay44205 Alpha-1 a
14	791	37.1	394	2	AAY44201	Aay44201 Alpha-1 a
15	791	37.1	418	2	AAR22931	Aar22931 Alpha-1 a
16	790	37.1	394	2	AAR67363	Aar67363 Alpha-1-a
17	790	37.1	394	2	AAR67360	Aar67360 Human alp
18	790	37.1	418	1	AAP50021	Aap50021 Sequence
19	787	36.9	394	2	AAR67362	Aar67362 Alpha-1-a
20	786	36.9	418	7	ADE60631	Ade60631 Human Pro
21	786	36.9	418	7	ADD45920	Add45920 Human Pro
22	786	36.9	418	8	ADK70484	Adk70484 Respirato
23	786	36.9	418	8	ADQ39557	Adq39557 Human myo
24	786	36.9	418	8	ADQ39553	Adq39553 Human myo
25	786	36.9	418	8	ADQ39558	Adq39558 Human myo
26	786	36.9	418	8	ADQ39559	Adq39559 Human myo
27	786	36.9	418	8	ADQ39555	Adq39555 Human myo
28	786	36.9	418	8	ADQ39556	Adq39556 Human myo
29	786	36.9	418	8	ADQ39554	Adq39554 Human myo
30	785.5	36.9	413	7	ADF28926	Adf28926 Rabbit al
31	785	36.9	394	2	AAW59839	Aaw59839 Mature pr
32	785	36.9	394	5	AAU99873	Aau99873 Human alp
33	785	36.9	394	6	ADA26998	Ada26998 Human alp
34	785	36.9	395	9	ADX59020	Adx59020 Human alp
35	785	36.9	398	8	ADM82878	Adm82878 Mouse alp
36	785	36.9	411	7	ADE63530	Ade63530 Rat Prote
37	785	36.9	411	7	ADE63526	Ade63526 Rat Prote
38	785	36.9	411	7	ADE63522	Ade63522 Rat Prote
39	785	36.9	411	7	ADE63534	Ade63534 Rat Prote
40	785	36.9	411	7	ADD45919	Add45919 Rat Prote
41	785	36.9	411	7	ADE60629	Ade60629 Rat Prote
42	785	36.9	418	1	AAP40133	Aap40133 Sequence
43	785	36.9	418	1	AAP94664	Aap94664 Predomina
44	785	36.9	418	2	AAY26925	Aay26925 Human alp
45	785	36.9	418	5	ABG96414	Abg96414 Human ova

ALIGNMENTS

RESULT 1
AAU05754
ID AAU05754 standard; protein; 414 AA.
XX
AC AAU05754;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human NOV7 polypeptide.
XX
KW Human; NOV7; AL132990 B; fertility disorder; spermatogenesis; cardiant;
KW cytostatic; immunomodulatory; antiproliferative; antidiabetic;
KW cell proliferation; cancer; diabetic retinopathy; angiogenic disorder;
KW pulmonary disorder; haematopoietic disorder; immunological disorder;
KW inflammatory disorder; tumour related disorders; emphysema; cirrhosis;
KW wound healing; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200149729-A2.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000299.
XX
PR 06-JAN-2000; 2000US-0174724P.
PR 11-JAN-2000; 2000US-0175434P.
PR 11-JAN-2000; 2000US-0175488P.
PR 12-JAN-2000; 2000US-0175696P.
PR 12-JAN-2000; 2000US-0175743P.
PR 13-JAN-2000; 2000US-0175819P.
PR 07-AUG-2000; 2000US-0223524P.
PR 04-JAN-2001; 2001US-00755665.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Prayaga SK, Majumder K, Taillon BE, Spaderna SK, Spytek KA;
PI Macdougall J;
XX
DR WPI; 2001-418356/44.
DR N-PSDB; AAS10874.
XX
PT Nucleic acids encoding polypeptides, designated NOVX polypeptides, useful
PT for treating a syndrome associated with a NOVX-associated disorder, e.g.
PT cell proliferation (e.g. cancer and diabetic retinopathy), angiogenic or
PT pulmonary disorder.
XX

PS Claim 1; Page 32; 144pp; English.
XX
CC The invention relates to nucleic acids encoding NOVX (X being an integer
CC from 1-8) polypeptides. The NOVX nucleic acids and polypeptides are
CC useful in diagnosing, treating or manufacturing a medicament for a
CC disease or disorder associated with NOVX e.g. cell proliferation (cancer
CC and diabetic retinopathy), angiogenic or pulmonary disorders, fertility
CC disorders (e.g of spermatogenesis), haematopoietic, immunological,
CC inflammatory and tumour related disorders, emphysema, cirrhosis, wound
CC healing. NOVX nucleic acids are also useful in gene therapy. They are
CC also used for screening for a modulator of activity or of latency or
CC predisposition to a NOVX-associated disorder. They are also useful for
CC determining the presence of or predisposition to a NOVX-associated
CC disorder. The present sequence represents NOV7 (AL132990 B), which has
CC sequence homology to an unidentified human secreted protein (HWHGUS54)
CC and to alpha1 anti-trypsin
XX
SQ Sequence 414 AA;

Query Match 100.0%; Score 2130; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 4.4e-181;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
Db 1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy 61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
Db 61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy 121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
Db 121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy 181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
Db 181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy 241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
Db 241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy 301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
Db 301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy 361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
Db 361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414

RESULT 2
AAE04885
ID AAE04885 standard; protein; 414 AA.
XX
AC AAE04885;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human protease protein-12 (PRTS-12).
XX
KW Human; protease protein-12; PRTS-12; cytostatic; hypotensive; antiviral;
KW gastrointestinal disorder; anorexia; dysphagia; cardiovascular disorder;
KW atherosclerosis; vasculitis; autoimmune disorder; inflammatory disorder;
KW Alzheimer's disease; cell proliferative disorder; dermatitis; cirrhosis;
KW acquired immune deficiency syndrome; AIDS; neurological disorder; asthma;
KW developmental disorder; epithelial disorder; eczema; dementia; nootropic;
KW neurological disorder; reproductive disorder; infertility; teratogenesis;
KW immunosuppressive; drug screening; actinic keratosis; cardiant; epilepsy;
KW anaemia; antitumour; gene therapy; antibacterial.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .19
FT /label= Signal_peptide
FT Protein 20. .414
FT /note= "Mature human PRTS-12"
XX
PN WO200146443-A2.
XX
PD 28-JUN-2001.
XX
PF 19-DEC-2000; 2000WO-US034811.
XX
PR 23-DEC-1999; 99US-0172055P.
PR 21-JAN-2000; 2000US-0177334P.
PR 28-JAN-2000; 2000US-0178884P.
PR 02-FEB-2000; 2000US-0179903P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Yang J, Baughn MR, Burford N, Au-Young J, Lu DAM, Reddy R;
PI Yue H, Nguyen DB, Tang YT, Yao MG, Lal P;
XX
DR WPI; 2001-418080/44.
DR N-PSDB; AAD09549.
XX
PT Novel human protease proteins (PRTS) useful for diagnosing, treating,
PT preventing gastrointestinal, cardiovascular, autoimmune/inflammatory,
PT cell proliferative disorders associated with abnormal expression of PRTS.
XX
PS Claim 1; Page 118; 129pp; English.
XX
CC The present sequence is human protease protein (PRTS-12). Human PRTS and
CC its nucleic acid molecule are useful for the diagnosis, treatment and
CC prevention of disorders associated with increased or decreased expression
CC of PRTS. Examples of such disorders include, gastrointestinal disorder
CC such as anorexia, dysphagia; cardiovascular disorder such as
CC atherosclerosis, vasculitis; autoimmune/inflammatory disorder such as
CC acquired immune deficiency syndrome (AIDS), asthma; cell proliferative
CC disorder such as actinic keratosis, cirrhosis; developmental disorder
CC such as epilepsy, anaemia; epithelial disorder such as allergic contact
CC dermatitis, eczema; neurological disorder such as Alzheimer's disease,
CC dementia and reproductive disorder such as infertility and teratogenesis.
CC PRTS DNA is useful for creating 'knockin' humanised animals (pigs) or
CC transgenic animals (mice or rats) to model human disease. PRTS DNA is
CC also in useful is gene therapy. PRTS and its immunogenic fragments are
CC useful for screening libraries of compounds in several drug screening
CC assays. PRTS is useful for analysing the proteome of a tissue or cell
CC type
XX
SQ Sequence 414 AA;

Query Match 100.0%; Score 2130; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 4.4e-181;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
Db 1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy 61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
Db 61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy 121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
Db 121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy 181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
Db 181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy 241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

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Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 3
ADA57300
ID   ADA57300 standard; protein; 414 AA.
XX
AC   ADA57300;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human secreted protein #583.
XX
KW   immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW   cytostatic; cerebroprotective; neuroprotective; nootropic;
KW   cardiovascular; antiarteriosclerotic; gene therapy;
KW   human secreted protein; immune disorder; inflammation;
KW   respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW   inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW   multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW   Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW   triple helix formation; antisense gene therapy; forensic biology.
XX
OS   Homo sapiens.
XX
PN   WO2002102994-A2.
XX
PD   27-DEC-2002.
XX
PF   19-MAR-2002; 2002WO-US008278.
XX
PR   21-MAR-2001; 2001US-0277340P.
PR   19-JUL-2001; 2001US-0306171P.
PR   13-NOV-2001; 2001US-0331287P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2003-167512/16.
DR   N-PSDB; ADA56404.
XX
PT   New human secreted polypeptides and polynucleotides, useful for
PT   diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT   conditions, respiratory disorders, cancers, CNS disorders, or
PT   neurodegenerative disorders.
XX
PS   Claim 13; SEQ ID NO 1490; 1754pp; English.
XX
CC   The invention relates to 592 new human secreted polypeptides useful for
CC   diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC   conditions, respiratory disorders, cancers, CNS disorders, or
CC   neurodegenerative disorders, or polypeptides comprising an amino acid
CC   sequence at least 95% identical to the new sequences. The polypeptides,
CC   antibodies or antibody fragments that bind to the polypeptides, nucleic
CC   acids encoding the polypeptides, agonists or antagonists that binds to
CC   the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC   compositions for diagnosing, treating or preventing an e.g. immune
CC   disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC   nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC   allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC   (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
CC   disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC   cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC   polynucleotides are useful for chromosome identification, chromosome
CC   mapping, for controlling gene expression through triple helix formation
CC   or antisense DNA or RNA, in gene therapy, for identifying individuals
CC   from minute biological samples, in forensic biology, and as hybridization
CC   probes. The polypeptides are useful for as molecular weight markers on
CC   sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC   gels, to raise antibodies, for testing biological activities, and for
CC   treating or preventing neural disorders, immune system disorders,
CC   muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC   renal, proliferative and/or cancerous diseases. This sequence corresponds
CC   to one of the polypeptide of the invention. Note: The sequence data for
CC   this patent did form part of the printed specification, but was obtained
CC   in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 414 AA;

  Query Match             100.0%;  Score 2130;  DB 6;  Length 414;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-181;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 4
ADA41179
ID   ADA41179 standard; protein; 414 AA.
XX
AC   ADA41179;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human secreted protein.
XX
KW   Human; secreted protein; cancer; hyperproliferative disorder;
KW   rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW   anaemia; allergic reaction; asthma; cardiovascular disorder;
KW   wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
KW   antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW   vulnerary; cardiant; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO2002102993-A2.
XX
PD   27-DEC-2002.
XX
```

PF 19-MAR-2002; 2002WO-US008123.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-175238/17.
XX
PT New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing,
PT preventing or treating cancer or other hyperproliferative disorder,
PT asthma, allergies or AIDS.
XX
PS Claim 1; SEQ ID NO 1561; 3205pp; English.
XX
CC The invention relates to novel genes ADA39629-ADA40565 and proteins
CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
CC treating or ameliorating medical conditions e.g. by protein or gene
CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
CC fragments, and agonists or antagonists that bind to the polypeptide are
CC useful for preparing a diagnostic or pharmaceutical composition for
CC diagnosing or treating cancer or other hyperproliferative disorder. The
CC polypeptides and nucleic acid molecules are also useful for detecting,
CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
CC or other hyperproliferative disorders including neoplasms, autoimmune
CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
CC thrombocytopenia), allergic reactions including asthma or eczema,
CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
CC fungal or viral infections including HIV/AIDS), or wound healing and
CC disorders of epithelial cell proliferation. The nucleic acids are also
CC useful for chromosome identification, radiation hybrid mapping or long-
CC range restriction mapping, as molecular weight markers, or as
CC hybridization or diagnostic probes. The polypeptides and antibodies are
CC useful for providing immunological probes for differential identification
CC of the tissues immunohistochemistry assays. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 414 AA;

Query Match 100.0%; Score 2130; DB 6; Length 414;
Best Local Similarity 100.0%; Pred. No. 4.4e-181;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
```

RESULT 5
ADN05952
ID ADN05952 standard; protein; 414 AA.
XX
AC ADN05952;
XX
DT 01-JUL-2004 (first entry)
XX
DE Antipsoriatic protein sequence #1136.
XX
KW antipsoriatic; gene therapy; psoriasis; diagnosis.
XX
OS Homo sapiens.
XX
PN WO2004028479-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030907.
XX
PR 25-SEP-2002; 2002US-0414006P.
XX
PA (GETH) GENENTECH INC.
XX
PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;
XX
DR WPI; 2004-305105/28.
DR N-PSDB; ADN05951.
XX
PT New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
XX
PS Claim 9; SEQ ID NO 2347; 3069pp; English.
XX
CC The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.
XX
SQ Sequence 414 AA;

Query Match 100.0%; Score 2130; DB 8; Length 414;
Best Local Similarity 100.0%; Pred. No. 4.4e-181;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
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Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 6
AAY86217
ID   AAY86217 standard; protein; 415 AA.
XX
AC   AAY86217;
XX
DT   19-APR-2000  (first entry)
XX
DE   Human secreted protein HWHGU54, SEQ ID NO:132.
XX
KW   Human; secreted protein; cancer; tumour; developmental abnormality;
KW   foetal deficiency; blood disorder; immune system disorder; inflammation;
KW   autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW   schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW   atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW   digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
KW   therapy.
XX
OS   Homo sapiens.
XX
PN   WO9966041-A1.
XX
PD   23-DEC-1999.
XX
PF   15-JUN-1999;   99WO-US013418.
XX
PR   16-JUN-1998;   98US-0089507P.
PR   16-JUN-1998;   98US-0089508P.
PR   16-JUN-1998;   98US-0089509P.
PR   16-JUN-1998;   98US-0089510P.
PR   22-JUN-1998;   98US-0090112P.
PR   22-JUN-1998;   98US-0090113P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Ni J,  Rosen CA,  Wei Y,  Young PE,  Florence KA;
PI   Soppet DR,  Brewer LA,  Endress GA,  Carter KC,  Mucenski M,  Ebner R;
PI   Lafleur DW,  Olsen HS,  Shi Y,  Moore PA,  Komatsoulis G;
XX
DR   WPI; 2000-106100/09.
DR   N-PSDB; AAZ97021.
XX
PT   New isolated human genes and the secreted polypeptides they encode,
PT   useful for diagnosis and treatment of e.g. cancers, neurological
PT   disorders, immune diseases, inflammation or blood disorders.
XX
PS   Claim 1; Page 389-390; 586pp; English.
XX
CC   AAZ97019 to AAZ97137 represent 94 isolated human secreted protein genes.
CC   AAY86215 to AAY86333 are the secreted proteins encoded by the 94 human
CC   genes. This sequence represents a fragment of one of the human secreted
CC   proteins. The genes and their corresponding secreted polypeptides are
CC   useful for preventing, treating or ameliorating medical conditions, e.g.,
CC   by protein or gene therapy. Also pathological conditions can be diagnosed
CC   by determining the amount of the new polypeptides in a sample or by
CC   determining the presence of mutations in the new genes. Specific uses are
CC   described for each of the 94 genes, based on which tissues they are most
CC   highly expressed in, and include developing products for the diagnosis or
CC   treatment of cancer, tumours, developmental abnormalities and foetal
CC   deficiencies, blood disorders, diseases of the immune system, autoimmune
CC   diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
CC   schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
CC   atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
CC   digestive/endocrine disorders, infections and AIDS. The polypeptides are
CC   also useful for identifying their binding partners. The sequences shown
CC   in AAY86334 to AAY86585 represent fragments of the secreted proteins
XX
SQ   Sequence 415 AA;

  Query Match           100.0%;  Score 2130;  DB 3;  Length 415;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-181;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 7
ABO53360
ID   ABO53360 standard; protein; 415 AA.
XX
AC   ABO53360;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Novel human secreted protein #3.
XX
KW   Human; vaccine; immune system disorder; haematopoietic cell disorder;
KW   cancer; autoimmune disorder; rheumatoid arthritis; glomerulonephritis;
KW   HIV infection; anaemia; thrombocytopenia blood coagulation disorder;
KW   blood platelet disorder; wound; heart attack; myocardial infarction;
KW   stroke; scarring; asthma; graft-versus host rejection; inflammation;
KW   hyperproliferative disorder; lymphoproliferative disorder; arrhythmia;
KW   aberrant cellular division; cell proliferative disorder; angiogenesis;
KW   cardiovascular disorder; pulmonary heart disease; neovascularisation;
KW   hypertrophic scar; keloid; ocular disorder; diabetic retinopathy;
KW   uveitis; epithelial cell proliferation; neurological disease; apoptosis;
KW   Parkinson's disease; Alzheimer's disease; Huntington's chorea; ALS; AIDS;
KW   amyotrophic lateral sclerosis; toxin induced liver disease; septic shock;
KW   cachexia; anorexia; lung damage; infection.
XX
OS   Homo sapiens.
XX
PN   US2003065151-A1.
XX
PD   03-APR-2003.
XX
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PF 04-APR-2002; 2002US-00115123.
XX
PR 16-JUN-1998; 98US-0089507P.
PR 16-JUN-1998; 98US-0089508P.
PR 16-JUN-1998; 98US-0089509P.
PR 16-JUN-1998; 98US-0089510P.
PR 22-JUN-1998; 98US-0090112P.
PR 22-JUN-1998; 98US-0090113P.
PR 15-JUN-1999; 99WO-US013418.
PR 14-DEC-1999; 99US-00461325.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Ni J, Rosen CA, Wei Y, Young P, Florence K, Soppet DR;
PI Brewer LA, Endress GA, Carter KC, Mucenski M, Ebner R, Lafleur DW;
PI Olsen H, Shi Y, Moore PA, Komatsoulis G;
XX
DR WPI; 2003-531736/50.
DR N-PSDB; ACH66650.
XX
PT Novel antibody that binds specifically to a HCEJQ69 protein, useful for
PT detecting the presence of a protein in a biological sample, and for
PT treating cancers, autoimmune disorders and HIV infection.
XX
PS Disclosure; SEQ ID NO 134; 176pp; English.
XX
CC The invention relates to an isolated antibody or its fragment that
CC specifically binds to a protein. The antibody is useful for detecting a
CC protein in a biological sample, by contacting the biological sample with
CC the antibody or its fragment and detecting the protein in the biological
CC sample. The antibody is useful for purifying, detecting and targeting the
CC human secreted proteins, including both in vitro and in vivo diagnostic
CC and therapeutic methods. The antibody is useful for immunophenotyping of
CC cell lines in biological samples and in antibody-based therapies for
CC treating, inhibiting and preventing diseases, disorders or conditions
CC associated with aberrant expression and/or activity of the above
CC proteins. The antibody is useful for treating deficiencies or disorders
CC of immune system and haematopoietic cells, for increasing differentiation
CC and proliferation of haematopoietic cells, for treating immune
CC deficiencies or disorders e.g. cancers, autoimmune disorders (such as
CC rheumatoid arthritis and glomerulonephritis), HIV infection, anaemia and
CC thrombocytopenia and as a marker for a particular immune system disease
CC or disorder. The antibody is also useful for treating blood coagulation
CC disorders, blood platelet disorders, wounds, heart attacks (infarction),
CC strokes, scarring and asthma. The antibody is also useful for treating or
CC preventing graft-versus host rejection, for modulating inflammation, for
CC treating hyperproliferative disorders e.g. lymphoproliferative disorders
CC and cancers, for inhibiting aberrant cellular division and for treating
CC cell proliferative disorders. The antibody is also useful for treating
CC cardiovascular disorders e.g. pulmonary heart disease and arrhythmia,
CC disorders associated with neovascularisation and angiogenesis, for
CC treating hypertrophic scars and keloids, ocular disorders e.g. diabetic
CC retinopathy and uveitis, for wound healing and disorders of epithelial
CC cell proliferation. The antibody is also useful for treating neurological
CC diseases e.g. Parkinson's disease, Alzheimer's disease, Huntington's
CC chorea and amyotrophic lateral sclerosis (ALS), diseases associated with
CC increased apoptosis e.g. AIDS, toxin induced liver disease, septic shock,
CC cachexia and anorexia, for preventing and healing damage to lungs and for
CC treating infectious diseases. The present sequence represents the amino
CC acid sequence of a novel human secreted protein. Note: the sequence data
CC for this patent did not form part of the printed specification but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030065151
XX
SQ Sequence 415 AA;

Query Match 100.0%; Score 2130; DB 6; Length 415;
Best Local Similarity 100.0%; Pred. No. 4.4e-181;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
```

RESULT 8
AAM78898
ID AAM78898 standard; protein; 414 AA.
XX
AC AAM78898;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1560.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR N-PSDB; AAK52031.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
PS Claim 20; Page 3878-3879; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the

CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 414 AA;

Query Match 99.7%; Score 2123; DB 4; Length 414;
Best Local Similarity 99.8%; Pred. No. 1.8e-180;
Matches 413; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVNKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
```

RESULT 9
ABB11832
ID ABB11832 standard; peptide; 431 AA.
XX
AC ABB11832;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human secreted protein homologue, SEQ ID NO:2202.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnerary; antiulcer.
XX
OS Homo sapiens.
XX
PN WO200157188-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US003800.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-457740/49.
DR N-PSDB; ABA09076.
XX
PT Human proteins and DNA encoding sequences useful for preventing, treating
PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
PT and cancer.
XX
PS Claim 20; Page 263; 1963pp; English.
XX
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a novel human
CC polypeptide of the invention
XX
SQ Sequence 431 AA;

Query Match 99.2%; Score 2114; DB 4; Length 431;
Best Local Similarity 99.3%; Pred. No. 1.2e-179;
Matches 411; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         18 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 77

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         78 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 137

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 197

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 IESKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 257

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 317

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        318 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVNKAELKM 377

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 431
```

```
RESULT 10
AAM79882
ID   AAM79882 standard; protein; 431 AA.
XX
AC   AAM79882;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human protein SEQ ID NO 3528.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US004098.
XX
PR   03-FEB-2000; 2000US-00496914.
PR   27-APR-2000; 2000US-00560875.
PR   20-JUN-2000; 2000US-00598075.
PR   19-JUL-2000; 2000US-00620325.
PR   01-SEP-2000; 2000US-00654936.
PR   15-SEP-2000; 2000US-00663561.
PR   20-OCT-2000; 2000US-00693325.
PR   30-NOV-2000; 2000US-00728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y;
PI   Ma Y,  Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   N-PSDB; AAK53015.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT   in diagnosis and gene therapy.
XX
PS   Claim 20; Page 371; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC   (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC   sequence listing were missing at the time of publication
XX
SQ   Sequence 431 AA;

  Query Match             99.2%;  Score 2114;  DB 4;  Length 431;
  Best Local Similarity   99.3%;  Pred. No. 1.2e-179;
  Matches  411;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         18 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 77

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 137

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 197

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 IESKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 257

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 317

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        318 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVNKAELKM 377

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 431
```

```
RESULT 11
AAU05759
ID   AAU05759 standard; protein; 358 AA.
XX
AC   AAU05759;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human NOV7 polypeptide #2.
XX
KW   Human; NOV7; AL132990 B; fertility disorder; spermatogenesis; cardiant;
KW   cytostatic; immunomodulatory; antiproliferative; antidiabetic;
KW   cell proliferation; cancer; diabetic retinopathy; angiogenic disorder;
KW   pulmonary disorder; haematopoietic disorder; immunological disorder;
KW   inflammatory disorder; tumour related disorders; emphysema; cirrhosis;
KW   wound healing; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 311. .322
FT                   /label= OTHER
FT                   /note= "Other= Unknown"
XX
PN   WO200149729-A2.
XX
PD   12-JUL-2001.
XX
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PF   05-JAN-2001; 2001WO-US000299.
XX
PR   06-JAN-2000; 2000US-0174724P.
PR   11-JAN-2000; 2000US-0175434P.
PR   11-JAN-2000; 2000US-0175488P.
PR   12-JAN-2000; 2000US-0175696P.
PR   12-JAN-2000; 2000US-0175743P.
PR   13-JAN-2000; 2000US-0175819P.
PR   07-AUG-2000; 2000US-0223524P.
PR   04-JAN-2001; 2001US-00755665.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Prayaga SK,  Majumder K,  Taillon BE,  Spaderna SK,  Spytek KA;
PI   Macdougall J;
XX
DR   WPI; 2001-418356/44.
XX
PT   Nucleic acids encoding polypeptides, designated NOVX polypeptides, useful
PT   for treating a syndrome associated with a NOVX-associated disorder, e.g.
PT   cell proliferation (e.g. cancer and diabetic retinopathy), angiogenic or
PT   pulmonary disorder.
XX
PS   Disclosure; Page 33; 144pp; English.
XX
CC   The invention relates to nucleic acids encoding NOVX (X being an integer
CC   from 1-8) polypeptides. The NOVX nucleic acids and polypeptides are
CC   useful in diagnosing, treating or manufacturing a medicament for a
CC   disease or disorder associated with NOVX e.g. cell proliferation (cancer
CC   and diabetic retinopathy), angiogenic or pulmonary disorders, fertility
CC   disorders (e.g of spermatogenesis), haematopoietic, immunological,
CC   inflammatory and tumour related disorders, emphysema, cirrhosis, wound
CC   healing. NOVX nucleic acids are also useful in gene therapy. They are
CC   also used for screening for a modulator of activity or of latency or
CC   predisposition to a NOVX-associated disorder. They are also useful for
CC   determining the presence of or predisposition to a NOVX-associated
CC   disorder. The present sequence represents a version of NOV7 (AL132990 B)
CC   appearing in table 25 of the specification, which has sequence homology
CC   to an unidentified human secreted protein (HWHGUS54) and to alpha1 anti-
CC   trypsin
XX
SQ   Sequence 358 AA;

  Query Match             83.7%;  Score 1783;  DB 4;  Length 358;
  Best Local Similarity   96.6%;  Pred. No. 3.3e-150;
  Matches  346;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLH 113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLH 60

Qy        114 EGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMA 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMA 120

Qy        174 QKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKN 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKN 180

Qy        234 SSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFS 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFS 240

Qy        294 RWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 RWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 300

Qy        354 HKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              ||||||||||          ||||||||||||||||||||||||||||||||||||
Db        301 HKAELKMDERXXXXXXXXXXXXXLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 358


RESULT 12
AAP50877
ID   AAP50877 standard; protein; 418 AA.
XX
AC   AAP50877;
XX
DT   25-MAR-2003  (revised)
DT   16-AUG-2002  (revised)
DT   03-SEP-1991  (first entry)
XX
DE   Sequence encoded by human alpha-1-antitrypsin (alpha-1-AT) cDNA.
XX
KW   Leukocyte elastase inhibitor; emphysema therapy; lung disease.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 125
FT                   /note= "Arg in published SQ"
FT   Misc-difference 139
FT                   /note= "Asp in published SQ"
FT   Misc-difference 140
FT                   /note= "Gly in published SQ"
FT   Misc-difference 237
FT                   /note= "Ala in published SQ"
FT   Misc-difference 273
FT                   /note= "Asn in published SQ"
FT   Misc-difference 326
FT                   /note= "Val in published SQ"
FT   Region          382. .383
FT                   /label= Reactive centre
XX
PN   EP164719-A.
XX
PD   18-DEC-1985.
XX
PF   14-JUN-1984;   84US-00620408.
XX
PR   14-JUN-1984;   84US-00620408.
PR   14-JUN-1984;   84US-00620662.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Barr PJ,  Hallewell RA,  Rosenberg S,  Brake AJ;
XX
DR   WPI; 1985-318257/51.
DR   N-PSDB; AAN50540.
XX
PT   Polypeptide oxidative stable serine protease inhibitor - having human
PT   alpha-1-antitrypsin amino-acid sequence with neutral amino-acid at active
PT   site.
XX
PS   Example; Page 16; 37pp; English.
XX
CC   The inventors claim a polypeptide oxidative stable human leukocyte
CC   elastase inhibitor differing from wild type human alpha-1-AT by fewer
CC   than 10 AAs and having the methionine at the active site (see AAP50877)
CC   substituted with a neutral oxidatively stable AA, pref. Val or Ala.
CC   (Updated on 16-AUG-2002 to add missing OS field.) (Updated on 25-MAR-2003
CC   to correct PA field.)
XX
SQ   Sequence 418 AA;

  Query Match             37.3%;  Score 795;  DB 1;  Length 418;
  Best Local Similarity   43.0%;  Pred. No. 6.3e-62;
  Matches  156;  Conservative   74;  Mismatches  131;  Indels    2;  Gaps    1;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
              :  | | ::|| ::    ||| ||:||:|||:|| || :  | ||| :| ||   ::||
Db         56 EFAFSLYRQLAHHSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQ 115

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
              :||||  ::| | |    |:|: || ||: : |:   ||||| |  | :|    || : |
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```
Db        116 IHEGFQQLLHTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTE 175

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
              |:||||||:: : | ||| :|:: :|  ||  | |||||: :|:  |:   |:|||| ::
Db        176 EAKKQINDYVEKGTQGKIVDLVKELDRHTVFALVNYIFFKGKWERPFEVKDTEEEDFHVD 235

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
              : ::|||||| | |:: : :  ||| :| : |  | |||| |||||||:|||  |  |
Db        236 QVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 295

Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
               :::     ||   : :|:| :|||:|||  |  :|::|:|    ||: :     ||: :
Db        296 ITKFLENEDRRSASLHLPKLSITGTYDLKSILGQLGITKVFSNGADLSGVTEQAPLKLSK 355

Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              ||||| | :||:||| |     : :||  |  || :||:: |:  :   | ||:||:|||
Db        356 AVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNP 415

Qy        412 IGK 414
               |
Db        416 TQK 418


RESULT 13
AAY44205
ID   AAY44205 standard; protein; 394 AA.
XX
AC   AAY44205;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Alpha-1 antitrypsin variant Pittsburgh.
XX
KW   Alpha-1 antitrypsin variant Pittsburgh; alpha-1 antitrypsin; PIT;
KW   negative control; furin inhibition assay; peptide mimetic; A7 cell;
KW   Pseudomonas aeruginosa exotoxin A; PEA; HCMV glycoprotein gB.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 358
FT                   /note= "Wild type Met substituted by Arg"
XX
PN   WO9951624-A1.
XX
PD   14-OCT-1999.
XX
PF   08-APR-1999;   99WO-US007776.
XX
PR   08-APR-1998;   98US-0081034P.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI   Jean F,  Thomas G;
XX
DR   WPI; 1999-620190/53.
XX
PT   New furin endoprotease inhibitor that mimics a specific region of alpha1-
PT   antitrypsin Portland mutant, for treatment and prevention of bacterial
PT   and viral infection.
XX
PS   Example 1; Page 101-102; 108pp; English.
XX
CC   The present sequence is alpha-1 antitrypsin mutated variant Pittsburgh
CC   (also termed PIT). PIT protein was used as a negative control in furin
CC   inhibition assay to assess the biological activity of the peptide
CC   mimetics. A7 cells when incubated with PIT exhibited little or no
CC   protective effect in the presence of Pseudomonas aeruginosa exotoxin A.
CC   PIT was also used as a negative control for the assay to detect PDX -
CC   mediated inhibition of furin-catalysed maturation of HCMV glycoprotein gB
XX
SQ   Sequence 394 AA;


  Query Match            37.2%;  Score 792;  DB 2;  Length 394;
  Best Local Similarity  43.0%;  Pred. No. 1.1e-61;
  Matches  156;  Conservative   72;  Mismatches  133;  Indels    2;  Gaps    1;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
              :  | | ::||  :   ||| ||:||:|||:|| || :  | ||| :| ||   ::||
Db         32 EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTQIPEAQ 91

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
              :|||| ::  | |     |:|: || ||: | |:   ||||| |  | :|    || : |
Db         92 IHEGFQELLRTLNQPDSQLQLTTGNGLFLSQGLKLVDKFLEDVKKLYHSEAFTVNFGDTE 151

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
              |:|||||:: : | ||| :|:: :|  ||  | |||||: :|:  |:   |:|||| ::
Db        152 QAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVD 211

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
              : ::|||||| | |:: : :  ||| :| : |  | |||| |||||||:|||  |  |
Db        212 QVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 271

Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
               :::     ||   : :|:| :|||:|||  |  :|::|:|    ||: :     ||: :
Db        272 ITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSK 331

Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              ||||| | :||:||| |     : :|   |  || :||:: |:  :   | ||:||:|||
Db        332 AVHKAVLTIDEKGTEAAGAMFLEAIPRSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNP 391

Qy        412 IGK 414
               ||
Db        392 TGK 394


RESULT 14
AAY44201
ID   AAY44201 standard; protein; 394 AA.
XX
AC   AAY44201;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Alpha-1 antitrypsin variant Portland.
XX
KW   Alpha-1 antitrypsin variant Portland; alpha-1 antitrypsin; PDX;
KW   protease inhibitor; furin endoprotease; peptide mimetic; bacterial toxin;
KW   furin recognition site; portland protein; SYBYL program; pharmacophore;
KW   protein crystal structure analysis; reactive site loop; RSL;
KW   endolytic maturation; endoproteolytic activation; Pseudomonas aeruginosa;
KW   Corynebacterium diptheriae; Bacillus anthracis; cytomegalovirus;
KW   biologically active protein.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 355
FT                   /note= "Wild type Ala substituted by Arg"
FT   Misc-difference 358
FT                   /note= "Wild type Met substituted by Arg"
XX
PN   WO9951624-A1.
XX
PD   14-OCT-1999.
XX
PF   08-APR-1999;   99WO-US007776.
XX
PR   08-APR-1998;   98US-0081034P.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI   Jean F,  Thomas G;
XX
```

```
DR   WPI; 1999-620190/53.
XX
PT   New furin endoprotease inhibitor that mimics a specific region of alpha1-
PT   antitrypsin Portland mutant, for treatment and prevention of bacterial
PT   and viral infection.
XX
PS   Claim 1; Page 98-99; 108pp; English.
XX
CC   The present sequence is alpha-1 antitrypsin mutated variant Portland
CC   (also termed PDX). This effectively inhibits furin endoprotease. Peptides
CC   or peptide mimetics derived from this sequence inhibit bacterial toxins
CC   that are processed at a consensus furin recognition site, when
CC   administered in therapeutically effective amounts. Portland protein
CC   generated by the SYBYL program and the crystal structure analysed for
CC   designing the pharmacophore for the reactive site loop of the Portland
CC   variant. Endoproteolytic activation of bacterial toxins and endolytic
CC   maturation of viral proteins is blocked by the peptide and peptide
CC   mimetics. This is useful in treating infections of cells by bacteria
CC   (specifically Corynebacterium diptheriae, Bacillus anthracis and
CC   Pseudomonas aeruginosa) or viruses (specifically cytomegalovirus). It may
CC   also be used to inhibit processing of biologically active proteins
XX
SQ   Sequence 394 AA;

  Query Match             37.1%;  Score 791;  DB 2;  Length 394;
  Best Local Similarity   43.0%;  Pred. No. 1.3e-61;
  Matches  156;  Conservative   72;  Mismatches  133;  Indels    2;  Gaps    1;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
              :  | | ::||  :   ||| ||:||:|||:|| || :  | ||| :| ||   ::||
Db         32 EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTQIPEAQ 91

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
              :||||  ::  | |    |:|: || ||: | |:   ||||| |  | :|    || : |
Db         92 IHEGFQELLRTLNQPDSQLQLTTGNGLFLSQGLKLVDKFLEDVKKLYHSEAFTVNFGDTE 151

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
              |:|||||:: : | ||| :|:: :|  ||  | |||||: :|:  |:   |:|||| ::
Db        152 QAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVD 211

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
              : ::|||||| | |:: : :  |||  :| : |  | |||| |||||||:|||  |  |
Db        212 QVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 271

Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
               :::     ||   : :|:| :|||:|||  |  :|::|:|    ||: :    ||: :
Db        272 ITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSK 331

Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              ||||| | :||:||| |     : :|   |  || :||:: |:  :   | ||:||:|||
Db        332 AVHKAVLTIDEKGTEAAGAMFLERIPRSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNP 391

Qy        412 IGK 414
              ||
Db        392 TGK 394


RESULT 15
AAR22931
ID   AAR22931 standard; protein; 418 AA.
XX
AC   AAR22931;
XX
DT   25-MAR-2003  (revised)
DT   23-SEP-1992  (first entry)
XX
DE   Alpha-1 antitrypsin cDNA sequence.
XX
KW   Alpha-1 AT; liver.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Cleavage-site   24. .25
FT   Misc-difference 125
FT                   /note= "Arg in known sequence"
FT   Misc-difference 139
FT                   /note= "Asp in known sequence"
FT   Misc-difference 140
FT                   /note= "Gly in known sequence"
FT   Misc-difference 237
FT                   /note= "Ala in known sequence"
FT   Misc-difference 273
FT                   /note= "Asn in known sequence"
FT   Misc-difference 326
FT                   /note= "Val in known sequence"
FT   Region          382. .384
FT                   /note= "reactive centre"
XX
PN   EP480480-A.
XX
PD   15-APR-1992.
XX
PF   03-MAY-1985;   91EP-00121606.
XX
PR   11-MAY-1984;   84US-00609540.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Rosenberg S,  Tekampolso P;
XX
DR   WPI; 1992-125144/16.
DR   N-PSDB; AAQ23746.
XX
PT   Preparation of construct producing high yields of polypeptide - utilising
PT   hybrid yeast promoters of glycolytic enzymes, for expression in yeast
PT   hosts.
XX
PS   Disclosure; Page 15; 23pp; English.
XX
CC   The sequence was deduced from the cDNA sequence obtd. by screening a cDNA
CC   library, constructed from polyA+ RNA from human liver, with two synthetic
CC   oligonucleotide probes based on the N- and C- terminal sequences of the
CC   partial sequence of alpha-1 antitrypsin (Kurachi et al., Proc. Natl.
CC   Acad. Sci. USA (1981) 78:6826; Leicht et al., Nature (1982) 297:655).
CC   Differences in protein sequence from published sequences are given in the
CC   feature table. (Updated on 25-MAR-2003 to correct PF field.) (Updated on
CC   25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI
CC   field.)
XX
SQ   Sequence 418 AA;

  Query Match             37.1%;  Score 791;  DB 2;  Length 418;
  Best Local Similarity   43.0%;  Pred. No. 1.4e-61;
  Matches  156;  Conservative   73;  Mismatches  132;  Indels    2;  Gaps    1;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
              :  | | ::||  :   ||| ||:||:|||:|| || :  | ||| :| ||   ::||
Db         56 EFAFSLYRQLAQQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQ 115

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
              :||||  ::| | |    |:|: || ||: : |:   ||||| |  | :|    || : |
Db        116 IHEGFQELLHTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTE 175

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
              |:|||||:: : | ||| :|:: :|  ||  | |||||: :|:  |:   |:|||| ::
Db        176 EAKKQINDYVEKGTQGKIVDLVKELDTDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVD 235

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
              : ::|||||| | |:: : :  |||  :| : |  | |||| |||||||:|||  |  |
Db        236 QVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 295

Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
               :::     ||   : :|:| :|||:|||  |  :|::|:|    ||: :    ||: :
Db        296 ITKFLENEDRRSASLHLPKLSITGTYDLKSILGQLGITKVFSNGADLSGVTEEAPLKLSK 355
```

```
Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              ||||| | :||:||| |     : :||  |  || :||:: |:  :   | ||:||:|||
Db        356 AVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNP 415

Qy        412 IGK 414
              |
Db        416 TQK 418
```

Search completed: March 31, 2006, 09:46:07
Job time : 192 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 09:46:24 ; Search time 41 Seconds
(without alignments)
971.555 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 2130
Sequence: 1 MNPTLGLAIFLAVLLTVKGL.....YSEKIPSVLFLGKIVNPIGK 414

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	787	36.9	409	1	ITBA	alpha-1-antitrypsi
2	785.5	36.9	413	2	S54981	alpha-1-antiprotei
3	785	36.9	411	1	ITRT	alpha-1-antitrypsi
4	785	36.9	418	1	ITHU	alpha-1-antitrypsi
5	782	36.7	406	2	JX0346	alpha-1-antiprotei
6	780.5	36.6	413	2	JX0154	alpha-1-antiprotei
7	778.5	36.5	413	2	JX0267	alpha-1-antiprotei
8	775.5	36.4	413	2	A54968	alpha-1-antitrypsi
9	768.5	36.1	413	2	I49470	alpha-1 proteinase
10	766.5	36.0	413	2	I49472	alpha-1 proteinase
11	760.5	35.7	413	2	I49452	alpha-1-antitrypsi
12	758.5	35.6	413	2	I49473	alpha-1 proteinase
13	756	35.5	402	2	I49471	alpha-1 proteinase
14	753	35.4	413	2	S60036	alpha-1-antitrypsi
15	747.5	35.1	408	2	S11320	serine proteinase
16	745.5	35.0	416	2	B29131	kallikrein-binding
17	743	34.9	403	2	S08102	serine proteinase
18	742.5	34.9	413	2	I49474	alpha-1 proteinase
19	742	34.8	416	2	S21097	alpha-1-antitrypsi
20	731	34.3	418	1	S31507	serine proteinase
21	728.5	34.2	406	2	A39339	protein C inhibito
22	728	34.2	416	1	ITSH	alpha-1-antitrypsi
23	726.5	34.1	418	2	JH0494	alpha-1-antichymot
24	725.5	34.1	410	2	A45457	alpha 1-proteinase
25	717	33.7	405	2	A39088	alpha-1-antiprotei
26	716	33.6	383	2	A36117	corticosteroid-bin
27	714	33.5	413	2	I56481	alpha 1-proteinase
28	710.5	33.4	418	2	S23675	contrapsin-related
29	707	33.2	412	1	ITMSC	alpha-1-antitrypsi
30	702	33.0	418	2	JX0129	contrapsin precurs
31	701	32.9	412	2	S31505	serine proteinase
32	701	32.9	417	2	S19724	kallikrein-binding
33	698.5	32.8	415	2	A47224	thyroxine-binding
34	696	32.7	430	2	A49190	corticosteroid-bin
35	686	32.2	412	2	I46421	thyroxine-binding
36	685.5	32.2	418	2	A39567	thyroxine-binding
37	684.5	32.1	406	2	I53281	corticosteroid-bin
38	680	31.9	410	2	C39088	contrapsin precurs
39	678.5	31.9	433	1	ITHUC	alpha-1-antichymot
40	674	31.6	405	2	A28321	corticosteroid-bin
41	663	31.1	410	2	I50494	serine proteinase
42	651.5	30.6	388	2	B39088	alpha-1-antiprotei
43	644.5	30.3	436	2	A42440	estrogen-regulated
44	629	29.5	427	2	A49518	kallistatin precur
45	620.5	29.1	369	2	JH0493	alpha-1-antichymot

ALIGNMENTS

RESULT 1
ITBA
alpha-1-antitrypsin precursor - baboon (fragment)
N;Alternate names: alpha-1-proteinase inhibitor
C;Species: Papio sp. (baboon)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 05-Oct-2004
C;Accession: A01248
R;Kurachi, K.; Chandra, T.; Degen, S.J.F.; White, T.T.; Marchioro, T.L.; Woo, S.L.C.; Da
Proc. Natl. Acad. Sci. U.S.A. 78, 6826-6830, 1981
A;Title: Cloning and sequence of cDNA coding for alpha-1-antitrypsin.
A;Reference number: A01248; MUID:82082539; PMID:7031661
A;Accession: A01248
A;Molecule type: mRNA
A;Residues: 1-409 <KUR>
A;Cross-references: UNIPARC:UPI0000124FDC; GB:J00321; NID:g176561; PIDN:AAA35377.1; PID:
C;Comment: Alpha-1-antitrypsin is an inhibitor of serine proteinases. Its primary target
psin.
C;Superfamily: serpin
C;Keywords: acute phase; glycoprotein; plasma; serine proteinase inhibitor
F;1-15/Domain: signal sequence (fragment) #status predicted <SIG>
F;16-409/Product: alpha-1-antitrypsin #status predicted <MAT>
F;61,98,262/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;373/Inhibitory site: Met (elastase, collagenase) #status predicted

Query Match 36.9%; Score 787; DB 1; Length 409;
Best Local Similarity 41.9%; Pred. No. 8e-47;
Matches 152; Conservative 82; Mismatches 127; Indels 2; Gaps 1;

```
Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
              :  | | ::||  :   ||| ||:||:|||:|| || :  |  || :| ||   ::||
Db         47 EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHSEILEGLNFNLTEIPEAQ 106

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
              :||||  ::  | :    |:|: || ||::: |:   ||||| || | :|    ||:: |
Db        107 VHEGFQELLRTLNKPDSQLQLTTGNGLFLNKSLKVVDKFLEDVKNLYHSEAFSVNFEDTE 166

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
              |:||||::: : | ||: :|:: :|  ||  | |||||: :|:  |:  |:|||| ::
Db        167 EAKKQINNYVEKGTQGKVVDLVKELDRDTVFALVNYIFFKGKWERPFEVEATEEEDFHVD 226

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
              : ::|||||| | |:: : : :|||  :| : |  | |||| |||||||:|||  |  |
Db        227 QATTVKVPMMRRLGMFNIYHCEKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 286

Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
               :::   :||  :: :|:| :|||:|||  | ::|::|:|    ||: :     ||: :
Db        287 ITKFLENENRRSANLHLPKLAITGTYDLKTVLGHLGITKVFSNGADLSGVTEDAPLKLSK 346

Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              ||||| | :||:||| |     : :||  |  || :||:: |:  :   | ||:||:|||
Db        347 AVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFIGKVVNP 406
```

```
Qy        412 IGK 414
                |
Db        407 TQK 409
```

RESULT 2
S54981
alpha-1-antiproteinase isoform E precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 05-Oct-2004
C;Accession: S54981; S72199
R;Saito, A.; Sinohara, H.
Biochem. J. 307, 369-375, 1995
A;Title: Rabbit alpha-1-antiproteinase E: a novel recombinant serpin which does not inhi
A;Reference number: S54981; MUID:95251597; PMID:7733871
A;Accession: S54981
A;Molecule type: mRNA
A;Residues: 1-413 <SAI1>
A;Cross-references: UNIPROT:Q28665; UNIPARC:UPI0000086790; EMBL:D17725; NID:g1008927; PI
A;Accession: S72199
A;Molecule type: protein
A;Residues: 25-33;374-387 <SAI2>
A;Cross-references: UNIPARC:UPI0000176311; UNIPARC:UPI0000176312
C;Superfamily: serpin
C;Keywords: acute phase; emphysema; glycoprotein; plasma; serine proteinase inhibitor
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-413/Product: alpha-1-antiproteinase E #status experimental <MAT>

  Query Match 36.9%; Score 785.5; DB 2; Length 413;
  Best Local Similarity 37.5%; Pred. No. 1e-46;
  Matches 155; Conservative 98; Mismatches 155; Indels 5; Gaps 2;

```
Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              | |::  |:   :||   | | | |     :  :     :   |  :|   :   |
Db          1 MPPSVSRAL---LLLAGLGCLLPGFLADEAQETAVSSHEQDHPACHRIAPSLAEFALSLY 57

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQG--FNFRKMPEKDLHEGFHY 118
              :::|  :   ||| ||:||: ||:|| |||:  |  :: :|  ||  :  |  :|:|| :
Db         58 REVAHESNTTNIFFSPVSIALAFAMLSLGAKGDTHTQVLEGLKFNLTETAEAQIHDGFRH 117

Qy        119 IIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQIN 178
              ::| : :   :|:|: || | : : |: | |||||||| | :|  | :|:: | |: :||
Db        118 LLHTVNRPDSELQLAAGNALVVHENLKLQHKFLEDAKNLYQSEAFLVDFRDPEQAKTKIN 177

Qy        179 DFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKV 238
                : : | ||| :|:: :|  |:: | ||:||: :|:  :|  |||||| ::  ::|:|
Db        178 SHVEKGTRGKIVDLVQELDARTLLALVNYVFFKGKWEKPFEPENTKEEDFHVDATTTVRV 237

Qy        239 PMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTL 298
              ||| | |:| : :   |: |:| : |: | ||:|:|||||||:|||  |  :  :::
Db        238 PMMSRLGMYVMFHCSTLASTVLRMDYKGNATALFLLPDEGKLQHLEDTLTTELIAKFLAK 297

Qy        299 LSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAEL 358
              | | | |  |:| ::||:|||  |  :|::::|  : ||: |     ||| :|:||| |
Db        298 SSLRSVTVRFPKLSISGTYDLKPLLGKLGITQVFSNNADLSGITEQEPLKVSQALHKAVL 357

Qy        359 KMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              :|||||| |  :  : :|   |  : :|:|:|: :||| :| | ||:||:|:|
Db        358 TIDERGTEAAGASFVELIPESVPDSITLDRPFLFVIYSHEIKSPLFVGKVVDP 410
```

RESULT 3
ITRT
alpha-1-antitrypsin precursor - rat
N;Alternate names: alpha-1-proteinase inhibitor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1992 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
C;Accession: A33892; B33892; S08016; JX0123; A38823
R;Chao, S.; Chai, K.X.; Chao, L.; Chao, J.
Biochemistry 29, 323-329, 1990
A;Title: Molecular cloning and primary structure of rat alpha-1-antitrypsin.
A;Reference number: A33892; MUID:90148955; PMID:2302382
A;Accession: A33892
A;Molecule type: mRNA
A;Residues: 4-411 <CHA>
A;Cross-references: UNIPROT:P17475; UNIPARC:UPI0000170896; GB:M32247; NID:g203062; PIDN:
A;Accession: B33892
A;Molecule type: protein
A;Residues: 25-57 <CH2>
A;Cross-references: UNIPARC:UPI00001731F9
R;Flink, I.L.; Bailey, T.; Morkin, E.
submitted to the EMBL Data Library, August 1989
A;Reference number: S08016
A;Accession: S08016
A;Molecule type: mRNA
A;Residues: 188-246,'I',248-321,'D',323-389 <FLI>
A;Cross-references: UNIPARC:UPI0000170B27; EMBL:X16273; NID:g57299; PIDN:CAA34349.1; PID:
R;Misumi, Y.; Sohda, M.; Ohkubo, K.; Takami, N.; Oda, K.; Ikehara, Y.
J. Biochem. 108, 230-234, 1990
A;Title: Molecular cloning and sequencing of the cDNA of rat alpha-1-protease inhibitor
A;Reference number: JX0123; MUID:91035351; PMID:2229024
A;Accession: JX0123
A;Molecule type: mRNA
A;Residues: 1-13,'G',15-83,'V',85-247,'Y',249-317,'N',319-411 <MIS>
A;Cross-references: UNIPARC:UPI000016797B; GB:D00675; NID:g220648; PIDN:BAA00579.1; PID:
A;Experimental source: serum
A;Accession: A38823
A;Molecule type: protein
A;Residues: 25-45 <MI2>
A;Cross-references: UNIPARC:UPI00001731FA
C;Comment: Alpha-1-antitrypsin is an inhibitor of serine proteinases. Its primary target
psin.
C;Superfamily: serpin
C;Keywords: acute phase; glycoprotein; plasma; serine proteinase inhibitor
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-411/Product: alpha-1-antitrypsin #status experimental <MAT>
F;64,101,265/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;376/Inhibitory site: Met (elastase, collagenase) #status predicted

  Query Match 36.9%; Score 785; DB 1; Length 411;
  Best Local Similarity 38.8%; Pred. No. 1.1e-46;
  Matches 161; Conservative 94; Mismatches 150; Indels 10; Gaps 5;

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Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              | |::   :  |   |      | |||   : :  ::      |    ::::     |  | |
Db          1 MAPSISRGLLLLAALC---CLAPSFLAEDAQE-TDTSQQDQSPTYRKISSNLADFAFSLY 56

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQG--FNFRKMPEKDLHEGFHY 118
              ::|   :   ||| ||:||:|||:|| ||::  |  :| :|  ||  ::|| |:|: ||:
Db         57 RELVHQSNTSNIFFSPMSITTAFAMLSLGSKGDTRKQILEGLEFNLTQIPEADIHKAFHH 116

Qy        119 IIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQIN 178
              ::  |  :   :|:|: || ||::: |:   ||||: || | :|    || : | |:| ||
Db        117 LLQTLNRPDSELQLNTGNGLFVNKNLKLVEKFLEEVKNNYHSEAFSVNFADSEEAKKVIN 176

Qy        179 DFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKV 238
              |:: : | ||| :|:: :|  ||  | |||||: :||  |:|  |:: || ::|:::|||
Db        177 DYVEKGTQGKIVDLMKQLDEDTVFALVNYIFFKGKWKRPFNPEHTRDADFHVDKSTTVKV 236

Qy        239 PMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTL 298
              ||| | |:: : |    ||  :| : |  | ||||:|||:||::|||:  |   |  ||:  |
Db        237 PMMNRLGMFDMHYCSTLSSWVLMMDYLGNATAIFLLPDDGKMQHLEQTLTKDLISRF--L 294

Qy        299 LSR--RVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKA 356
              |:|  |   :  |:| ::||::||  || :|::::|    ||: |     ||: :|||||
Db        295 LNRQTRSAILYFPKLSISGTYNLKTLLSSLGITRVFNNDADLSGITEDAPLKLSQAVHKA 354

Qy        357 ELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              | :|||||| |  |  : :||  |  || | |:: :|   :  | ||:||:::|
Db        355 VLTLDERGTEAAGATVVEAVPMSLPPQVKFDHPFIFMIVESETQSPLFVGKVIDP 409
```

RESULT 4
ITHU
alpha-1-antitrypsin precursor [validated] - human
N;Alternate names: alpha-1-AT; alpha-1-proteinase inhibitor

C;Species: Homo sapiens (man)
C;Date: 30-Nov-1980 #sequence_revision 31-Mar-1992 #text_change 05-Oct-2004
C;Accession: A21853; B21853; A93352; A90944; A58528; A23174; A93281; A32336; S14476; A24
R;Long, G.L.; Chandra, T.; Woo, S.L.C.; Davie, E.W.; Kurachi, K.
Biochemistry 23, 4828-4837, 1984
A;Title: Complete sequence of the cDNA for human alpha-1-antitrypsin and the gene for th
A;Reference number: A21853; MUID:85047190; PMID:6093867
A;Accession: A21853
A;Molecule type: mRNA
A;Residues: 1-418 <LON1>
A;Cross-references: UNIPROT:P01009; UNIPARC:UPI000000CBEC; GB:K02212; NID:g177830
A;Experimental source: M (normal) allele
A;Accession: B21853
A;Molecule type: DNA
A;Residues: 1-287,'V',289-418 <LON2>
A;Cross-references: UNIPARC:UPI000016A3A8; GB:K02212; NID:g177830; PIDN:AAB59495.1; PID:
A;Experimental source: S variant allele
R;Rosenberg, S.; Barr, P.J.; Najarian, R.C.; Hallewell, R.A.
Nature 312, 77-80, 1984
A;Title: Synthesis in yeast of a functional oxidation-resistant mutant of human alpha-1-
A;Reference number: A93352; MUID:85036645; PMID:6387509
A;Accession: A93352
A;Molecule type: mRNA
A;Residues: 1-124,'H',126-325,'I',327-418 <ROS>
A;Cross-references: UNIPARC:UPI0000141DE5; EMBL:X01683; NID:g28965
R;Bollen, A.; Herzog, A.; Cravador, A.; Herion, P.; Chuchana, P.; Vander Straten, A.; Lo
DNA 2, 255-264, 1983
A;Title: Cloning and expression in Escherichia coli of full-length complementary DNA cod
A;Reference number: A90944; MUID:84107980; PMID:6319097
A;Accession: A90944
A;Molecule type: mRNA
A;Residues: 1-138,'DG',141-272,'N',274-418 <BOL>
A;Cross-references: UNIPARC:UPI00001731EF; GB:K01396; NID:g28965
A;Note: this sequence has been corrected in reference A58528
R;Colau, B.; Chuchana, P.; Bollen, A.
DNA 3, 327-330, 1984
A;Title: Revised sequence of full-length complementary DNA coding for human alpha-1-anti
A;Reference number: A58528; MUID:85026667; PMID:6333329
A;Contents: corrections to sequence in A90944
A;Accession: A58528
A;Molecule type: mRNA
A;Residues: 1-418 <COL>
A;Cross-references: UNIPARC:UPI000000CBEC; GB:K01396; NID:g28965; PIDN:CAA25838.1; PID:g
R;Ciliberto, G.; Dente, L.; Cortese, R.
Cell 41, 531-540, 1985
A;Title: Cell-specific expression of a transfected human alpha-1-antitrypsin gene.
A;Reference number: A23174; MUID:85176977; PMID:2985281
A;Accession: A23174
A;Molecule type: mRNA
A;Residues: 1-11,13-173,'H',175-228,'D',230-418 <CIL>
A;Cross-references: UNIPARC:UPI000016A3A7; GB:M11465; NID:g177826; PIDN:AAA51546.1; PID:
A;Note: the authors state that this sequence corresponds to the M (normal) allele; 3 var
R;Carrell, R.W.; Jeppsson, J.O.; Laurell, C.B.; Brennan, S.O.; Owen, M.C.; Vaughan, L.;
Nature 298, 329-334, 1982
A;Title: Structure and variation of human alpha-1-antitrypsin.
A;Reference number: A93281; MUID:82220135; PMID:7045697
A;Accession: A93281
A;Molecule type: protein
A;Residues: 25-418 <CAR>
A;Cross-references: UNIPARC:UPI000014E111
A;Note: peptide sequence differences with A21853 (Leu-200 and the amidation states of re
R;Zhu, X.J.; Kang, S.S.; Hargrove, K.; Shochat, D.; Jarrells, M.; Mojesky, M.; Chan, S.K
Biochem. J. 246, 25-36, 1987
A;Title: The identification of epitopic sites in human alpha-1-proteinase inhibitor.
A;Reference number: A32336; MUID:88049621; PMID:2445337
A;Accession: A32336
A;Molecule type: protein
A;Residues: 25-418 <ZHU>
A;Cross-references: UNIPARC:UPI000014E111
A;Note: peptides were sequenced or partially sequenced and ordered by comparison with A2
R;Weiland, K.L.; Falany, C.N.; Dooley, T.P.
submitted to the EMBL Data Library, December 1989
A;Description: Identification of a cDNA encoding a variant form of the human proteolytid

A;Reference number: S14476
A;Accession: S14476
A;Molecule type: mRNA
A;Residues: 142-230,'Y',232-338 <WEI>
A;Cross-references: UNIPARC:UPI000006E0F9; EMBL:X17122; NID:g28636; PIDN:CAA34982.1; PID
A;Experimental source: a variant form
R;Riley, J.H.; Bathurst, I.C.; Edbrooke, M.R.; Carrell, R.W.; Craig, R.K.
FEBS Lett. 189, 361-366, 1985
A;Title: Alpha-1-antitrypsin and serum albumin mRNA accumulation in normal, acute phase
A;Reference number: A24013; MUID:86005469; PMID:3876243
A;Accession: A24013
A;Molecule type: mRNA
A;Residues: 292-418 <RIL>
A;Cross-references: UNIPARC:UPI000016A3A9; EMBL:X02920; NID:g24437; PIDN:CAA26677.1; PID
R;Schulze, A.J.; Baumann, U.; Knof, S.; Jaeger, E.; Huber, R.; Laurell, C.B.
Eur. J. Biochem. 194, 51-56, 1990
A;Title: Structural transition of alpha(1)-antitrypsin by a peptide sequentially similar
A;Reference number: S13833; MUID:91071209; PMID:2253623
A;Accession: S13833
A;Molecule type: protein
A;Residues: 25-41 <SCH>
A;Cross-references: UNIPARC:UPI00001731F0
R;Niemann, M.A.; Narkates, A.J.; Miller, E.J.
Matrix 12, 233-241, 1992
A;Title: Isolation and serine protease inhibitory activity of the 44-residue, C-terminal
A;Reference number: S23516; MUID:93024095; PMID:1406456
A;Accession: S23516
A;Molecule type: protein
A;Residues: 375-409,'L',411-413,'S' <NIE>
A;Cross-references: UNIPARC:UPI0000070F7B
R;Dengler, R.; Eger, G.; Lottspeich, F.; Plewan, A.; Ogilvie, A.; Emmerich, B.
Biol. Chem. Hoppe-Seyler 373, 581-588, 1992
A;Title: Proteolytic inactivation of alpha(1)-proteinase inhibitor in vivo: detection, c
A;Reference number: S23962; MUID:92384968; PMID:1515087
A;Accession: S23962
A;Molecule type: protein
A;Residues: 44-53;384-392 <DEN>
A;Cross-references: UNIPARC:UPI00001731F1; UNIPARC:UPI00001731F2
R;Dengler, R.; Lottspeich, F.; Oberthuer, W.; Mast, A.E.; Emmerich, B.
Biol. Chem. Hoppe-Seyler 376, 165-172, 1995
A;Title: Limited proteolysis of alpha(1)-proteinase inhibitor (alpha(1)-PI) in acute leu
A;Reference number: S55249; MUID:95336645; PMID:7612193
A;Accession: S55249
A;Molecule type: protein
A;Residues: 25-28;43-47;207-208;382-389;414-418 <DE2>
A;Cross-references: UNIPARC:UPI00001583FA; UNIPARC:UPI00001731F3; UNIPARC:UPI00001731F4;
R;Leicht, M.; Long, G.L.; Chandra, T.; Kurachi, K.; Kidd, V.J.; Mace, M.
Nature 297, 655-659, 1982
A;Title: Sequence homology and structural comparison between the chromosomal human alpha
A;Reference number: I39371; MUID:82220035; PMID:6979715
A;Accession: I39371
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-67 <LEI1>
A;Cross-references: UNIPARC:UPI000016A3A5; GB:J00064; NID:g177817; PIDN:AAB59369.1; PID:
A;Accession: I39372
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 196-225 <LEI2>
A;Cross-references: UNIPARC:UPI000016A3A6; GB:J00066; NID:g177819; PIDN:AAB59370.1; PID:
R;Chang, W.S.W.; Wardell, M.R.; Lomas, D.A.; Carrell, R.W.
Biochem. J. 314, 647-653, 1996
A;Title: Probing serpin reactive-loop conformations by proteolytic cleavage.
A;Reference number: S63599; MUID:96239126; PMID:8670081
A;Accession: S63599
A;Molecule type: protein
A;Residues: 371-385 <CHA>
A;Cross-references: UNIPARC:UPI00001731F7
R;Coutelle, C.; Speer, A.; Rogers, J.; Kalsheker, N.; Humphries, S.; Williamson, R.
Biomed. Biochim. Acta 44, 421-431, 1985
A;Title: Construction and partial characterization of a human liver cDNA library.
A;Reference number: I39370; MUID:85225507; PMID:3873938
A;Accession: I39370

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 387-399,'D',401-418 <COU>
A;Cross-references: UNIPARC:UPI000016A3A4; GB:M26123; NID:g177815; PIDN:AAA51545.1; PID:
R;Faber, J.P.; Weidinger, S.; Olek, K.
Am. J. Hum. Genet. 46, 1158-1162, 1990
A;Title: Sequence data of the rare deficient alpha-1-antitrypsin variant PI Zaugsburg.
A;Reference number: A35338; MUID:90252805; PMID:2339709
A;Accession: A35338
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 122-124,'H',126-128;363-365,'K',367-369 <FAB>
A;Cross-references: UNIPARC:UPI0000147271; UNIPARC:UPI00001731F8
A;Experimental source: mutant PI Zaugsberg
A;Note: this Z mutation with Lys-366 arose from the M2 variant with His-125
R;Loebermann, H.; Tokuoka, R.; Deisenhofer, J.; Huber, R.
submitted to the Brookhaven Protein Data Bank, September 1988
A;Reference number: A50775; PDB:7API
A;Contents: annotation; X-ray crystallography, 3.0 angstroms, tetragonal form 1, residue
R;Loebermann, H.; Tokuoka, R.; Deisenhofer, J.; Huber, R.
submitted to the Brookhaven Protein Data Bank, September 1988
A;Reference number: A50794; PDB:8API
A;Contents: annotation; X-ray crystallography, 3.1 angstroms, hexagonal form, residues 4
R;Loebermann, H.; Tokuoka, R.; Deisenhofer, J.; Huber, R.
submitted to the Brookhaven Protein Data Bank, September 1988
A;Reference number: A50810; PDB:9API
A;Contents: annotation; X-ray crystallography, 3.0 angstroms, tetragonal form 2, residue
R;Loebermann, H.; Tokuoka, R.; Deisenhofer, J.; Huber, R.
J. Mol. Biol. 177, 531-556, 1984
A;Title: Human alpha-1-proteinase inhibitor. Crystal structure analysis of two crystal m
A;Reference number: A58525; MUID:84292309; PMID:6332197
A;Contents: annotation; X-ray crystallography, 3.0 angstroms
R;Carrell, R.W.; Jeppsson, J.O.; Vaughan, L.; Brennan, S.O.; Owen, M.C.; Boswell, D.R.
FEBS Lett. 135, 301-303, 1981
A;Title: Human alpha-1-antitrypsin: carbohydrate attachment and sequence homology.
A;Reference number: A58526; MUID:82095611; PMID:6976274
A;Contents: annotation; carbohydrate attchment sites
C;Comment: The Z variant allele has Lys-366. Deficiency of the normal inhibitor in indiv
sis.
C;Genetics:
A;Gene: GDB:PI
A;Cross-references: GDB:120289; OMIM:107400
A;Map position: 14q32.1-14q32.1
A;Introns: 216/1; 306/2; 355/3
A;Note: the first intron occurs before the initiator codon
C;Function:
A;Description: inhibitor of serine proteinases, primarily leukocyte elastase and collage
A;Note: it also inhibits plasmin, thrombin, kallikrein, trypsin, and chymotrypsin
C;Superfamily: serpin
C;Keywords: acute phase; emphysema; glycoprotein; plasma; polymorphism; serine proteinas
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-418/Product: alpha-1-antitrypsin #status experimental <MAT>
F;70,107,271/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             36.9%;  Score 785;  DB 1;  Length 418;
  Best Local Similarity   42.7%;  Pred. No. 1.1e-46;
  Matches  155;  Conservative   73;  Mismatches  133;  Indels    2;  Gaps    1;

Qy         54 DLGPKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
              :  | | ::||  :   ||| ||:||:|||:|| || :  | ||| :| ||   ::||
Db         56 EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQ 115

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
              :|||| ::  | |    |:|: || ||: : |:   ||||| |  | :|    || : |
Db        116 IHEGFQELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTE 175

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
              |:|||||:: : | ||| :|:: :|  ||  | |||||: :|:  |:   |:|||| ::
Db        176 EAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVD 235

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
              : ::|||||| | |:: : :  |||  :| : |  | |||| |||||||:|||  |  |
Db        236 QVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 295

Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
              :::     ||  : :|:| :|||:|||  |  :|::|:|    ||: :     ||: :
Db        296 ITKPLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSK 355

Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              ||||| | :||:||| |     : :||  |  || :||:: |:  :   | ||:||:|||
Db        356 AVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNP 415

Qy        412 IGK 414
              |
Db        416 TQK 418


RESULT 5
JX0346
alpha-1-antiproteinase precursor - Mongolian jird
C;Species: Meriones unguiculatus (Mongolian jird)
C;Date: 22-Apr-1995 #sequence_revision 26-May-1995 #text_change 05-Oct-2004
C;Accession: JX0346; PC2357
R;Goto, K.; Suzuki, Y.; Yoshida, K.; Yamamoto, K.; Sinohara, H.
J. Biochem. 116, 582-588, 1994
A;Title: Plasma alpha-1-antiproteinase from the Mongolian gerbil, Meriones unguiculatus:
A;Reference number: JX0346; MUID:95155268; PMID:7852275
A;Accession: JX0346
A;Molecule type: mRNA
A;Residues: 1-406 <GOT>
A;Cross-references: UNIPROT:Q64118; UNIPARC:UPI00000E8496; GB:S77822; NID:g998663; PIDN:
A;Accession: PC2357
A;Molecule type: protein
A;Residues: 25-44;77-96 <GO2>
A;Cross-references: UNIPARC:UPI000017630E; UNIPARC:UPI000017630F
A;Experimental source: plasma
C;Superfamily: serpin
C;Keywords: glycoprotein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-406/Product: alpha-1-antiproteinase #status predicted <MAT>
F;383-387/Region: serpin binding #status predicted
F;59,96,134,260,403/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;371/Inhibitory site: Met (trypsin, chymotrypsin, elastase) #status predicted

  Query Match             36.7%;  Score 782;  DB 2;  Length 406;
  Best Local Similarity   41.3%;  Pred. No. 1.7e-46;
  Matches  166;  Conservative   84;  Mismatches  142;  Indels   10;  Gaps    4;

Qy         14 LLTVKGL--LKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRN 71
              || : ||  | |||    :  |       :  : |  ||    |  | | : |:  :   |
Db          9 LLLLAGLCCLVPSFLAED--AEKTDSSHQDHIMASNLA----DFAFGLYRVLSHQSNTTN 62

Qy         72 IFLSPLSISTAFSMLCLGAQDSTLDEIKQG--FNFRKMPEKDLHEGFHYIIHELTQKTQD 129
              ||||||||:|| :|| ||::| |  :: ||  ||  :  | |:|:|| :::  | :   :
Db         63 IFLSPLSIATALAMLSLGSKDDTKAQLLQGLHFNLTETSEADIHKGFQHLLKTLNRPDNE 122

Qy        130 LKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKI 189
              |:|: |::||::   |     ||||: || | :|    || : | |:| || |: : |||||
Db        123 LQLTTGSSLFVNNSLNLVEKFLEEVKNHYHSEAFFVNFADSEEAKKTINSFVEKATHGKI 182

Qy        190 NNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQV 249
              :|:::::  ||: | |||||| :|:  ||| :|:| || ::|:::|||||| | |:: |
Db        183 VDLVKDLEIDTVLALVNYIFFRGKWEKPFDPELTEEADFHVDKSTTVKVPMMNRMGMFDV 242

Qy        250 GYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVP 309
              | | ||  :| : |  | ||||||||||::|||: |  :   ::       |  :| :|
Db        243 HYCDTLSSWVLLMDYLGNATAIFILPDEGKMQHLEQTLTKEHIYKFLQNRHTRSANVHLP 302

Qy        310 RLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAA 369
              :| ::||::||| || :|::::|    ||: |     ||: :||||| | :|||||| |
Db        303 KLSISGTYNLKKVLSPLGITQVFSNGADLSGITTDVPLKLSKAVHKAVLTLDERGTEAAG 362

Qy        370 GTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              |  : :||  |  |    |::::|  :   | ||:||:|||
Db        363 TTVLEAVPMSIPPDVCFKNPFVVIICDKHTQSPLFVGKVVNP 404
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RESULT 6
JX0154
alpha-1-antiproteinase F - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 05-Oct-2004
C;Accession: JX0154
R;Saito, A.; Sinohara, H.
J. Biochem. 109, 158-162, 1991
A;Title: Cloning and sequencing of cDNA coding for rabbit alpha-1-antiproteinase F: amin
A;Reference number: JX0154; MUID:91201273; PMID:2016265
A;Accession: JX0154
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-413 <SAI>
A;Cross-references: UNIPROT:P23035; UNIPARC:UPI0000124FCE; GB:X57710; NID:g1455; PIDN:CA
C;Superfamily: serpin

Query Match 36.6%; Score 780.5; DB 2; Length 413;
Best Local Similarity 37.5%; Pred. No. 2.3e-46;
Matches 155; Conservative 96; Mismatches 157; Indels 5; Gaps 2;

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Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              | |::  |:   :||   | | | |     : :     :   | :|   :   |
Db          1 MPPSVSRAL---LLLAGLGCLLPGFLADEAQETAVSSHEQDHPACHRIAPSLAEFALSLY 57

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQG--FNFRKMPEKDLHEGFHY 118
              :::|  :   ||| ||:||: ||:|| |||:  |  :: :|  ||  :  |  :|:|| :
Db         58 REVAHESNTTNIFFSPVSIALAFAMLSLGAKGDTHTQVLEGLKFNLTETAEAQIHDGFRH 117

Qy        119 IIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQIN 178
              ::| : :   :|:|:  | | : : |: | |||||||| | :|  | :|:: | |: :||
Db        118 LLHTVNRPDSELQLAARNALVVHENLKLQHKFLEDAKNLYQSEAFLVDFRDPEQAKTKIN 177

Qy        179 DFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKV 238
              : : | ||| :|:: :|  |:: | ||:||: :|:  |:|  |||||| :  ::|:|
Db        178 SHVEKGTRGKIVDLVQELDARTLLALVNYVFFKGKWEKPFEPENTKEEDFHVNATTTVRV 237

Qy        239 PMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTL 298
              ||| | | | : :   |: |:| : |: | ||:|:|||||||:|||  |  :  :::
Db        238 PMMSRLGRYDLFHCSTLASTVLRMDYKGNATALFLLPDEGKLQHLEDTLTTELITKFLAK 297

Qy        299 LSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAEL 358
              | | | |  |:| ::||:|||  |  :|::::| :: ||: |     ||  :|:||| |
Db        298 SSLRSVTVHFPKLSISGTYDLKPLLGKLGITQVFSDNADLSGITEQEPLKASQALHKAVL 357

Qy        359 KMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              :|||||| |  |  : :||  |  : :|:|:| :||| :| | ||:||:|:|
Db        358 TIDERGTEAAGATYMEIIPMSLPDSITLDRPFLFVIYSHEIKSPLFVGKVVDP 410
```

RESULT 7
JX0267
alpha-1-antiproteinase S-1 precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
C;Accession: JX0267
R;Saito, A.; Sinohara, H.
J. Biochem. 113, 456-461, 1993
A;Title: Rabbit plasma alpha-1-antiproteinase s-1: cloning, sequencing, expression, and
A;Reference number: JX0267; MUID:93293795; PMID:8514734
A;Accession: JX0267
A;Molecule type: mRNA
A;Residues: 1-413 <SAI>
A;Cross-references: UNIPROT:Q07298; UNIPARC:UPI0000086E35; GB:D16104; NID:g286191; PIDN:
A;Experimental source: liver
A;Note: part of this sequence, including the amino end of the mature protein, was confir
C;Superfamily: serpin
C;Keywords: glycoprotein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-413/Product: alpha-1-antiproteinase S-1 #status experimental <MAT>
F;65,102,266/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 36.5%; Score 778.5; DB 2; Length 413;
Best Local Similarity 37.8%; Pred. No. 3.1e-46;
Matches 156; Conservative 95; Mismatches 157; Indels 5; Gaps 2;

```
Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              | |::  |:   :||   | | | |     : :     :   | :|   :   |
Db          1 MPPSVSRAL---LLLAGLGCLLPGFLADEAQETAVSSHEQDHPACHRIAPSLAEFALSLY 57

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQG--FNFRKMPEKDLHEGFHY 118
              :::|  :   ||| ||:||: ||:|| |||:  |  :: :|  ||  :  |  :|:|| :
Db         58 REVAHESNTTNIFFSPVSIALAFAMLSLGAKGDTHTQVLEGLKFNLTETAEAQIHDGFRH 117

Qy        119 IIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQIN 178
              ::| : :   :|:|:  || | : : |: | |||||||| | :|  | :|:: | |: :||
Db        118 LLHTVNRPDSELQLAAGNALVVHENLKLQHKFLEDAKNLYQSEAFLVDFRDPEQAKTKIN 177

Qy        179 DFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKV 238
              : : | ||| :|:: :|  |:: | ||:||: :|:  |:|  |||||| :  ::|:|
Db        178 SHVEKGTRGKIVDLVQELDARTLLALVNYVFFKGKWEKPFEPENTKEEDFHVDATTTVRV 237

Qy        239 PMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTL 298
              ||| | |:|  :   |: |:: : |: | ||:|:|||||||:|||  |  :  :::
Db        238 PMMSRLGMYVMFHCSTLASTVVLMDYKGNATALFLLPDEGKLQHLEHTLTTELIAKFLAK 297

Qy        299 LSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAEL 358
              | | | |  |:| ::||:|||  |  :|::::| :: ||: |     ||  :|:||| |
Db        298 SSFRSVRVRFPKLSISGTYDLKPLLGKLGITQVFSDNADLSGITEQEPLKVSQALHKAVL 357

Qy        359 KMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              :|||||| |  |  :|  |  :|:|:| :||| :| | ||:||:|:|
Db        358 TIDERGTEAAGATFVGIMPSSLPESVIFDRPFLFVIYSHELKSPLFVGKVVDP 410
```

RESULT 8
A54968
alpha-1-antitrypsin precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 05-Oct-2004
C;Accession: A54968
R;Ray, B.K.; Gao, X.; Ray, A.
J. Biol. Chem. 269, 22080-22086, 1994
A;Title: Expression and structural analysis of a novel highly inducible gene encoding alp
A;Reference number: A54968; MUID:94350954; PMID:8071331
A;Accession: A54968
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-413 <RAY>
A;Cross-references: UNIPROT:Q28666; UNIPARC:UPI00000876E0; GB:L12139; NID:g405551; PIDN:A
C;Superfamily: serpin

Query Match 36.4%; Score 775.5; DB 2; Length 413;
Best Local Similarity 37.3%; Pred. No. 5e-46;
Matches 154; Conservative 100; Mismatches 154; Indels 5; Gaps 2;

```
Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              | |::  |:   :||   | | | |     : :     :   | :|   :   |
Db          1 MPPSVSRAL---LLLAGLGCLLPGFLADEAQETAVSSHEQDRPACHRIAPSLVEFALSLY 57

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQG--FNFRKMPEKDLHEGFHY 118
              :::|  :   ||| ||:||: ||:|| |||:  |  :: :|  ||  :  |  :|:|| :
Db         58 REVARESNTTNIFFSPVSIALAFAMLSLGAKGDTHTQVLEGLKFNLTETAEAQIHDGFRH 117

Qy        119 IIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQIN 178
              ::| : :   :|:|:  || | : : |: | |||||||| | :|  | :|:: | |: :||
Db        118 LLHTVNRPDSELQLAAGNALVVSENLKLQHKFLEDAKNLYQSEAFLVDFRDPEQAKTKIN 177

Qy        179 DFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKV 238
              : : | ||| :|:: :|  |:: | ||:||: :|:  |:|  |||||| :  ::|:|
Db        178 SHVEKGTRGKIVDLVQELDARTLLALVNYVFFKGKWEKPFEPENTKEEDFHVDATTTVRV 237

Qy        239 PMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTL 298
              ||| | |:|  : :   |: |:: : |: | ||:|:|||||||:|||  |  :  :::
Db        238 PMMSRLGMYVMFHCSTLASTVVLMDYKGNATALFLLPDEGKLQHLEHTLTTELIAKFLAK 297
```

```
Qy        299 LSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAEL 358
Db        298 SSFRSVTVRFPKLSISGTYDLKPLLGKLGITQVFSDNADLSGITEQEALKVSQALHKVVL 357

Qy        359 KMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
Db        358 TIDERGTEAAGATFVEYVLYSMPQRVTFDRPFLFVIYSHEVKSPLFVGKVVDP 410


RESULT 9
I49470
alpha-1 proteinase inhibitor 1 - mouse
N;Alternate names: alpha-1-antitrypsin
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: I49470; A25495
R;Borriello, F.; Krauter, K.S.
Proc. Natl. Acad. Sci. U.S.A. 88, 9417-9421, 1991
A;Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary dive
A;Reference number: I49470; MUID:92052104; PMID:1946354
A;Accession: I49470
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-413 <RES>
A;Cross-references: UNIPROT:P07758; UNIPARC:UPI0000021AE6; GB:M75721; NID:g191841; PIDN:
R;Krauter, K.S.; Citron, B.A.; Hsu, M.T.; Powell, D.; Darnell Jr., J.E.
DNA 5, 29-36, 1986
A;Title: Isolation and characterization of the alpha-1-antitrypsin gene of mice.
A;Reference number: A25495; MUID:86163765; PMID:3007061
A;Accession: A25495
A;Molecule type: mRNA
A;Residues: 211-245,'D',247-322,'L',324-403,'V',405-413 <KRA>
A;Cross-references: UNIPARC:UPI000016CC23; GB:M12586; NID:g192092; PIDN:AAA51624.1; PID:
C;Genetics:
A;Gene: alpha-1 PI-1
C;Superfamily: serpin

  Query Match             36.1%;  Score 768.5;  DB 2;  Length 413;
  Best Local Similarity   39.4%;  Pred. No. 1.5e-45;
  Matches  165;  Conservative   85;  Mismatches  158;  Indels   11;  Gaps    5;

Qy          1 MNPTLGLAIFLAVLLTVKGL--LKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFK 58
Db          1 MTPSISWG-----LLLLAGLCCLVPSFLAEDVQETDTSQK-DQSPASHEIATNLGDFAIS 54

Qy         59 LLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQG--FNFRKMPEKDLHEGF 116
Db         55 LYRELVHQSNTSNIFFSPVSIATAFAMLSLGSKGDTHTQILEGLQFNLTQTSEADIHKSF 114

Qy        117 HYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQ 176
Db        115 QHLLQTLNRPDSELQLSTGNGLFVNNDLKLVEKFLEEAKNHYQAEVFSVNFAESEEAKKV 174

Qy        177 INDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSV 236
Db        175 INDFVEKGTQGKIAEAVKKLDQDTVFALANYILFKGKWKKPFDPENTEEAEFHVDESTTV 234

Qy        237 KVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWK 296
Db        235 KVPMMTLSGMLHVHHCSTLSSWVLLMDYAGNATAVFLLPDDGKMQHLEQTLSKELISKFL 294

Qy        297 TLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRS-LKVGEAVHK 355
Db        295 LNRRRRLAQIHFPRLSISGEYNLKTLMSPLGITRIFNNGADLSGITEENAPLKLSQAVHK 354

Qy        356 AELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
Db        355 AVLTIDETGTEAAAVTVLQMVPMSMPPILRFDHPFLFIIFEEHTQSPIFLGKVVDPTHK 413


RESULT 10
I49472
alpha-1 proteinase inhibitor 3 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: I49472
R;Borriello, F.; Krauter, K.S.
Proc. Natl. Acad. Sci. U.S.A. 88, 9417-9421, 1991
A;Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary dive
A;Reference number: I49470; MUID:92052104; PMID:1946354
A;Accession: I49472
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-413 <RES>
A;Cross-references: UNIPROT:Q00896; UNIPARC:UPI0000028CD4; GB:M75720; NID:g191845; PIDN:
C;Genetics:
A;Gene: alpha-1 PI-3
C;Superfamily: serpin

  Query Match             36.0%;  Score 766.5;  DB 2;  Length 413;
  Best Local Similarity   39.4%;  Pred. No. 2.1e-45;
  Matches  165;  Conservative   83;  Mismatches  160;  Indels   11;  Gaps    5;

Qy          1 MNPTLGLAIFLAVLLTVKGL--LKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFK 58
Db          1 MTPSISWG-----LLLLAGLCCLVPSFLAEDVQETDTSQK-DQSPASHEIATNLGDFAIS 54

Qy         59 LLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQG--FNFRKMPEKDLHEGF 116
Db         55 LYRELVHQSNTSNIFFSPVSIATAFAMLSLGSKGDTHTQILEGLQFNLTQTSEADIHKSF 114

Qy        117 HYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQ 176
Db        115 QHLLQTLNRPDSELQLSTGNGLFVNNDLKLVEKFLEEAKNHYQAEVFSVNFAESEEAKKV 174

Qy        177 INDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSV 236
Db        175 INDFVEKGTQGKIAEAVKKLDQDTVFALANYILFKGKWKKPFDPENTEEAEFHVDESTTV 234

Qy        237 KVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWK 296
Db        235 KVPMMTLSGMLDVHHCSTLSSWVLLMDYAGNATAVFLLPDDGKMQHLEQTLSKELISKFL 294

Qy        297 TLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRS-LKVGEAVHK 355
Db        295 LKRPRRLAQIHFPRLSISGEYNLKTLMSPLGITRIFNNGADLSGITEENAPLKLSQAVHK 354

Qy        356 AELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
Db        355 AVLTMDETGTEAAAATVLLAVPYSMPPIVRFDHPFLFIIFEEHTQSPLFVGKVVDPTHK 413


RESULT 11
I49452
alpha-1-antitrypsin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: I49452
R;Sifers, R.N.; Ledley, F.D.; Reed-Fourquet, L.; Ledbetter, D.H.; Ledbetter, S.A.; Woo,
Genomics 6, 100-104, 1990
A;Title: Complete cDNA sequence and chromosomal localization of mouse alpha-1-antitrypsi
A;Reference number: I49452; MUID:90152670; PMID:2303252
A;Accession: I49452
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-413 <RES>
A;Cross-references: UNIPROT:P22599; UNIPARC:UPI0000029619; GB:M25529; NID:g191549; PIDN:
C;Superfamily: serpin

  Query Match             35.7%;  Score 760.5;  DB 2;  Length 413;
  Best Local Similarity   39.2%;  Pred. No. 5.4e-45;
  Matches  165;  Conservative   88;  Mismatches  153;  Indels   15;  Gaps    7;

Qy          1 MNPTLGLAIFLAVLLTVKGL--LKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFK 58
```

```
Db          1 MTPSISWG-----LLLLAGLCCLVPSFLAEDVQETDTSQK-DQSPASHEIATNLGDFAIS 54

Qy         59 LLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQG--FNFRKMPEKDLHEGF 116

Db         55 LYRELVHQSNTSNIFFSPVSIATAFAMLSLGSKGDTHTQILEGLQFNLTQTSEADIHKSF 114

Qy        117 HYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQ 176

Db        115 QHLLQTLNRPDSELQLSTGNGLFVNNDLKLVEKFLEEAKNHYQAEVFSVNFAESEEAKKV 174

Qy        177 INDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSV 236

Db        175 INDFVEKGTQGKIVEAVKELDQDTVFALGNYILFKGKWKKPFDPENTEEAEFHVDKSTTV 234

Qy        237 KVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWK 296

Db        235 KVPMMTLSGMLDVHHCSTLSSWVLLMDYAGNASAVFLLPEDGKMQHLEQTLNKELIS--K 292

Qy        297 TLLS--RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRS-LKVGEAV 353

Db        293 ILLNRRRRLVQIHIPRLSISGEYNLKTLMSPLGITRIFNNGADLSGITEENAPLKLSKAV 352

Qy        354 HKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIG 413

Db        353 HKAVLTIDETGTEAAAATVFEAVPMSMPPILRFDHPFLFIIFEEHTQSPIFVGKVVDPTH 412

Qy        414 K 414
              |
Db        413 K 413
```

RESULT 12
I49473
alpha-1 proteinase inhibitor 4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: I49473
R;Borriello, F.; Krauter, K.S.
Proc. Natl. Acad. Sci. U.S.A. 88, 9417-9421, 1991
A;Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary dive
A;Reference number: I49470; MUID:92052104; PMID:1946354
A;Accession: I49473
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-413 <RES>
A;Cross-references: UNIPROT:Q00897; UNIPARC:UPI0000003E4C; GB:M75718; NID:g191847; PIDN:
C;Genetics:
A;Gene: alpha-1 PI-4
C;Superfamily: serpin

  Query Match 35.6%; Score 758.5; DB 2; Length 413;
  Best Local Similarity 39.4%; Pred. No. 7.4e-45;
  Matches 166; Conservative 87; Mismatches 153; Indels 15; Gaps 7;

```
Qy          1 MNPTLGLAIFLAVLLTVKGL--LKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFK 58

Db          1 MTPSISWS-----LLLLAGLCCLVPSFLAEDVQETDTSQK-DQSPASHEIATNLGDFALR 54

Qy         59 LLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQG--FNFRKMPEKDLHEGF 116

Db         55 LYRELVHQSNTSNIFFSPVSIATAFAMLSLGSKGDTHTQILEGLQFNLTQTSEADIHKSF 114

Qy        117 HYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQ 176

Db        115 QHLLQTLNRPDSELQLSTGNGLFVNNDLKLVEKFLEEAKNHYQAEVFSVNFAESEEAKKV 174

Qy        177 INDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSV 236

Db        175 INDFVEKGTQGKIVEAVKKLDQDTVFALANYILFKGKWKQPFDPENTEEAEFHVDESTTV 234

Qy        237 KVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWK 296

Db        235 KVPMMTLSGMLDVHHCSMLSSWVLLMDYAGNTTAVFLLPDDGKMQHLEQTLNKELISQF- 293

Qy        297 TLLSRRVVD--VSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRS-LKVGEAV 353

Db        294 -LLNRRRSDAQIHIPRLSISGNYNLKTLMSPLGITRIFNNGADLSGITEENAPLKLSKAV 352

Qy        354 HKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIG 413

Db        353 HKAVLTIDETGTEAAAATVLQVATYSMPPIVRFDHPFLFIIFEEHTQSPIFVGKVVDPTH 412

Qy        414 K 414
              |
Db        413 K 413
```

RESULT 13
I49471
alpha-1 proteinase inhibitor 2 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: I49471
R;Borriello, F.; Krauter, K.S.
Proc. Natl. Acad. Sci. U.S.A. 88, 9417-9421, 1991
A;Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary dive
A;Reference number: I49470; MUID:92052104; PMID:1946354
A;Accession: I49471
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-402 <RES>
A;Cross-references: UNIPROT:P22599; UNIPARC:UPI000016CBEA; GB:M75716; NID:g191843; PIDN:
C;Genetics:
A;Gene: alpha-1 PI-2
C;Superfamily: serpin

  Query Match 35.5%; Score 756; DB 2; Length 402;
  Best Local Similarity 40.1%; Pred. No. 1.1e-44;
  Matches 159; Conservative 85; Mismatches 145; Indels 8; Gaps 5;

```
Qy         23 PSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSISTA 82

Db          9 PSFLAEDVQETDTSQK-DQSPASHEIATNLGDFAISLYRELVHQSNTSNIFFSPVSIATA 67

Qy         83 FSMLCLGAQDSTLDEIKQG--FNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLFI 140

Db         68 FAMLSLGSKGDTHTQILEGLQFNLTQTSEADIHKSFQHLLQTLNRPDSELQLSTGNGLFV 127

Qy        141 DQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPGT 200

Db        128 NNDLKLVEKFLEEAKNHYQAEVFSVNFAESEEAKKVINDFVEKGTQGKIVEAVKELDQDT 187

Qy        201 VMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTIL 260

Db        188 VFALANYILFKGKWKKPFDPENTEEAEFHVDKSTTVKVPMMMLSGMLDVHHCSILSSWVL 247

Qy        261 EIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS--RRVVDVSVPRLHMTGTFD 318

Db        248 LMDYAGNASAVFLLPEDGKMQHLEQTLNKELIS--KILLNRRRRLVQIHIPRLSISGDYN 305

Qy        319 LKKTLSYIGVSKIFEEHGDLTKIAPHRS-LKVGEAVHKAELKMDERGTEGAAGTGAQTLP 377

Db        306 LKTLMSPLGITRIFNNGADLSGITEENAPLKLSKAVHKAVLTIDETGTEAAAATVFEAVP 365

Qy        378 METPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414

Db        366 MSMPPILRFDHPFLFIIFEEHTQSPIFVGKVVDPTHK 402
```

RESULT 14
S60036
alpha-1-antitrypsin precursor - golden hamster
N;Alternate names: alpha-1-antiproteinase
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 05-Oct-2004
C;Accession: S60036

```
R;Nakatani, T.; Suzuki, Y.; Yoshida, K.; Sinohara, H.
Biochim. Biophys. Acta 1263, 245-248, 1995
A;Title: Molecular cloning and sequence analysis of cDNA encoding plasma alpha-1-antiprc
A;Reference number: S60036; MUID:96004896; PMID:7548212
A;Accession: S60036
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-413 <NAK>
A;Cross-references: UNIPROT:P97277; UNIPARC:UPI00000E67E5; EMBL:D49709; NID:g1088432; PI
A;Note: the source is designated as Syrian hamster
C;Superfamily: serpin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-413/Product: alpha-1-antitrypsin #status predicted <MAT>

  Query Match             35.4%;  Score 753;  DB 2;  Length 413;
  Best Local Similarity   38.7%;  Pred. No. 1.8e-44;
  Matches  161;  Conservative   87;  Mismatches  158;  Indels   10;  Gaps    4;

Qy          1 MNPTLGLAIFLAVLLTVKGL--LKPSPSPRNYKALSEVQGWKQRMAAKELARQNMDLGFK 58
              | |::   | |     : ||  | |||   : :     :  ::  |  ::|    |  |
Db          1 MKPSISWGILL-----LAGLCCLVPSFLAEDAQETDASKQDQEHQACCKIAPNLADFSFN 55

Qy         59 LLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQ--GFNFRKMPEKDLHEGF 116
              | ::|   :   ||| ||:||:|||:|| || :  |  :| :  |||  :: | ::|:||
Db         56 LYRELVHQSNTTNIFFSPVSIATAFAMLSLGTKGVTHTQILEGLGFNLTEIAEAEVHKGF 115

Qy        117 HYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQ 176
              | ::    :   :|:|: || |||   |:   ||||: || | :|    || : | |:|
Db        116 HNLLQTFNRPDNELQLTTGNGLFIHNNLKLVDKFLEEVKNDYHSEAFSVNFTDSEEAKKV 175

Qy        177 INDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSV 236
              || |: : | ||| :|::::|  ||: | |||||: :||  || : |:| || ::| ::|
Db        176 INGFVEKGTQGKIVDLVKDLDKDTVLALVNYIFFKGKWKKPFDADNTEEADFHVDKTTTV 235

Qy        237 KVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWK 296
              |||||  |  |:: | |    ||  :| : |  | |||||||:||::|||: |  :   ::
Db        236 KVPMMSRLGMFDVHYVSTLSSWVLLMDYLGNATAIFILPDDGKMQHLEQTLNKEIIGKFL 295

Qy        297 TLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKA 356
                  |  :|  |:| ::||::||  |  :|::::|    ||: |     ||:|:|||||
Db        296 KDRHTRSANVHFPKLSISGTYNLKTALDPLGITQVFSNGADLSGITEDVPLKLGKAVHKA 355

Qy        357 ELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYS-EKIPSVLFLGKIVNP 411
              | :|||||| |  |  : :||  |  |  : |:: :||  :   | ||:||:|:|
Db        356 VLTIDERGTEAAGATFMEIIPMSVPPEVNFNSPFIAIIYDRQTAKSPLFVGKVVDP 411


RESULT 15
S11320
serine proteinase inhibitor 3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 05-Oct-2004
C;Accession: S11320; S08100
R;Pages, G.; Rouayrenc, J.F.; le Cam, G.; Mariller, M.; le Cam, A.
Eur. J. Biochem. 190, 385-391, 1990
A;Title: Molecular characterization of three rat liver serine-protease inhibitors affect
A;Reference number: S11318; MUID:90306038; PMID:1694763
A;Accession: S11320
A;Molecule type: mRNA
A;Residues: 1-408 <PAG>
A;Cross-references: UNIPARC:UPI0000167956; EMBL:X16359; NID:g57234; PIDN:CAA34408.1; PID
R;le Cam, A.
submitted to the EMBL Data Library, August 1989
A;Reference number: S08099
A;Accession: S08100
A;Molecule type: mRNA
A;Residues: 1-366 <LEC>
A;Cross-references: UNIPARC:UPI0000176300; EMBL:X16359
C;Superfamily: serpin

  Query Match             35.1%;  Score 747.5;  DB 2;  Length 408;
  Best Local Similarity   40.6%;  Pred. No. 4.2e-44;
  Matches  151;  Conservative   79;  Mismatches  133;  Indels    9;  Gaps    5;

Qy         48 LARQNMDLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQG--FNFR 105
              ||  | |  | | ||||  || :|:  ||||||  | ::: |||: |:::|| :|  ||
Db         37 LASINTDFAFSLYKKLALRNPHKNVVFSPLSISAALAVVSLGAKGSSMEEILEGLKFNLT 96

Qy        106 KMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILT 165
              : || ::| || :::  |:|   ::::| || |||::|||   :| | ||  | ||
Db         97 ETPETEIHRGFGHLLQRLSQPRDEIQISTGNALFIEKRLQVLAEFQEKAKALYQAEAFTA 156

Qy        166 NFQNLEMAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKE 225
              :||    |:| |||::|::| |||  || |:   | |:| |||:|: :||  |||  | :
Db        157 DFQQSREAKKLINDYVSKQTQGKIQGLITNLAKKTSMVLVNYIYFKGKWKVPFDPRDTFQ 216

Qy        226 EDFFLEKNSSVKVPMMFRSGIYQVGY--DDKLSCTILEIPYQKNITAIFILPDEGKLKHL 283
              :|:  |  |||||||    :    |  |::|:||::|: |  | :|:|||||:||:: :
Db        217 SEFYSGKRRSVKVPMMKLEDL-TTPYVRDEELNCTVVELKYTGNASALFILPDQGKMQQV 275

Qy        284 EKGLQVDTFSRWKTLLSRRVVD-VSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIA 342
              |  || :|  |||  |   ::| : :|:  ::  ::|:  |  :|: ::|    ||: |
Db        276 EASLQPETLRRWKDSLRPSMIDELYLPKFSISADYNLEDVLPELGIKEVFSTQADLSGIT 335

Qy        343 PHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPMET---PLVVKIDKPYLLLIYSEKI 399
              : | | : |||| | : | ||| || || : :||     ||::  |:|:|::|   :
Db        336 GDKDLMVFQVVHKAVLDVAETGTEAAAATGVKFVPMSAKLDPLIIAFDRPFLMIISDTET 395

Qy        400 PSVLFLGKIVNP 411
                 || || ||
Db        396 AIAPFLAKIFNP 407


Search completed: March 31, 2006, 09:50:51
Job time : 42 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 09:43:04 ; Search time 233 Seconds
(without alignments)
1253.600 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 2130
Sequence: 1 MNPTLGLAIFLAVLLTVKGL.....YSEKIPSVLFLGKIVNPIGK 414

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2130	100.0	414	2	Q8IW75_HUMAN	Q8iw75 homo sapien
2	1406	66.0	411	2	Q8R4Z1_RAT	Q8r4z1 rattus norv
3	1380	64.8	413	2	Q7TMF5_MOUSE	Q7tmf5 mus musculu
4	1378	64.7	413	2	Q9CQ32_MOUSE	Q9cq32 m mus muscu
5	1369	64.3	413	2	Q6P6M3_MOUSE	Q6p6m3 mus musculu
6	876.5	41.2	432	2	Q7SYX0_XENLA	Q7syx0 xenopus lae
7	857	40.2	431	2	Q66KX6_XENLA	Q66kx6 xenopus lae
8	857	40.2	433	2	Q9YIB8_XENLA	Q9yib8 xenopus lae
9	841	39.5	436	2	Q5M911_XENTR	Q5m911 xenopus tro
10	827	38.8	426	2	Q8JIA6_SPHPU	Q8jia6 sphenodon p
11	792	37.2	396	1	A1AT_CERAE	O00394 cercopithec
12	790	37.1	418	1	A1AT_PONPY	Q5rcw5 pongo pygma
13	787	36.9	409	1	A1AT_PAPAN	P01010 papio anubi
14	785.5	36.9	413	2	Q28665_RABIT	Q28665 oryctolagus
15	785	36.9	411	1	A1AT_RAT	P17475 rattus norv
16	785	36.9	418	1	A1AT_HUMAN	P01009 homo sapien
17	785	36.9	418	2	Q53XB8_HUMAN	Q53xb8 homo sapien
18	782	36.7	406	1	A1AT_MERUN	Q64118 meriones un
19	780.5	36.6	413	1	A1AF_RABIT	P23035 oryctolagus
20	778.5	36.5	413	2	Q07298_RABIT	Q07298 oryctolagus
21	775.5	36.4	413	2	Q28666_RABIT	Q28666 oryctolagus
22	772.5	36.3	456	2	O62663_RABIT	O62663 oryctolagus
23	772	36.2	411	2	Q9TTE1_BOVIN	Q9tte1 bos taurus
24	768.5	36.1	413	1	A1AT1_MOUSE	P07758 mus musculu
25	766.5	36.0	413	1	A1AT3_MOUSE	Q00896 mus musculu
26	766	36.0	417	2	Q5J801_BOVIN	Q5j801 bos taurus
27	764	35.9	415	2	Q9GMA6_PIG	Q9gma6 sus scrofa
28	763	35.8	421	1	A1AT_PIG	P50447 sus scrofa
29	762.5	35.8	413	1	A1AT2_MOUSE	P22599 mus musculu
30	761	35.7	412	1	A1AT_CALCN	O54763 callosciuru
31	758.5	35.6	413	1	A1AT4_MOUSE	Q00897 mus musculu
32	753	35.4	413	1	A1AT_MESAU	P97277 mesocricetu
33	752.5	35.3	412	1	A1AT6_MOUSE	P81105 mus musculu
34	752.5	35.3	420	2	Q60552_MESAU	Q60552 mesocricetu
35	752	35.3	421	1	A1AT2_HORSE	P38029 equus cabal
36	745.5	35.0	413	2	Q8VC41_MOUSE	Q8vc41 mus musculu
37	745	35.0	413	1	CPI3_RAT	P05544 rattus norv
38	743.5	34.9	418	1	CPI6_RAT	P09006 rattus norv
39	742.5	34.9	413	1	A1AT5_MOUSE	Q00898 mus musculu
40	742.5	34.9	413	2	Q545P1_MOUSE	Q545p1 mus musculu
41	742	34.8	416	1	A1AT_BOVIN	P34955 bos taurus
42	740	34.7	413	1	ALMS_SPETR	O54761 spermophilu
43	737.5	34.6	416	1	CPI1_RAT	P05545 r contrapsi
44	735	34.5	445	1	SPA3F_MOUSE	Q80x76 mus musculu
45	733	34.4	413	2	Q76HP0_TAMSI	Q76hp0 tamias sibi

ALIGNMENTS

RESULT 1
Q8IW75_HUMAN
ID Q8IW75_HUMAN PRELIMINARY; PRT; 414 AA.
AC Q8IW75;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Serine (Or cysteine) proteinase inhibitor, clade A (Alpha-1
DE antiproteinase, antitrypsin), member 12 (OL-64) (Visceral adipose-
DE specific SERPIN).
GN Name=SERPINA12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RG NIH MGC Project;
RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RA Chen S., Guo J.H., Yu L.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Hida K., Wada J., Zhang H.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

```
CC   -!- SIMILARITY: Belongs to the serpin family.
DR   EMBL; BC040857; AAH40857.1; -; mRNA.
DR   EMBL; AY177692; AAO18649.1; -; mRNA.
DR   EMBL; AY326420; AAP88384.1; -; mRNA.
DR   HSSP; P01009; 1QMB.
DR   Ensembl; ENSG00000165953; Homo sapiens.
DR   HGNC; HGNC:18359; SERPINA12.
DR   GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   Pfam; PF00079; Serpin; 1.
DR   SMART; SM00093; SERPIN; 1.
KW   Serpin.
SQ   SEQUENCE   414 AA;  47175 MW;  5C70F1AB5935661C CRC64;

  Query Match             100.0%;  Score 2130;  DB 2;  Length 414;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-143;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 2
Q8R4Z1_RAT
ID   Q8R4Z1_RAT  PRELIMINARY;      PRT;   411 AA.
AC   Q8R4Z1;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Visceral adipose tissue specific SERPIN.
GN   Name=Serpina12; Synonyms=Vaspin;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=OLETF; TISSUE=Visceral adipose;
RA   Hida K., Wada J., Zhang H., Shikata K., Makino H.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the serpin family.
DR   EMBL; AF245398; AAL99574.1; -; mRNA.
DR   HSSP; P01008; 1ATH.
DR   Ensembl; ENSRNOG00000009710; Rattus norvegicus.
DR   RGD; 708485; Serpina12.
DR   GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR   InterPro; IPR000295; Prot_inh_Lserp2.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   Pfam; PF00079; Serpin; 1.
DR   PRINTS; PR00780; LEUSERPINII.
DR   SMART; SM00093; SERPIN; 1.
KW   Serpin.
SQ   SEQUENCE   411 AA;  47527 MW;  29FA271FF8CC8A2D CRC64;

  Query Match             66.0%;  Score 1406;  DB 2;  Length 411;
  Best Local Similarity   62.8%;  Pred. No. 8.8e-92;
  Matches  258;  Conservative   84;  Mismatches   69;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||  ||| :||| ||||||||:   :|  |::   || |: :  |:|| | ||: |||||
Db          1 MNLVLGLGLFLAGLLTVKGLLQDRDAPDTYESPVRVQEWRGKKDARELTRHNMEFGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ::||  :   |||||||||||||||| ||||:|||:||::||||::| ::|:| ||||::
Db         61 QRLASNSRQGNIFLSPLSISTAFSMLSLGAQNSTLEEIREGFNFKEMSDRDMHMGFHYLL 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
               :| ::|||:|:|||| ||:||||:||::||: ||| | |: ||||||:||  || || :
Db        121 QKLNRETQDVKMSIGNALFMDQRLRPQQRFLKLAKNLYDADMILTNFQDLENTQKNINKY 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||:||| :| |:::|||||||||| |||:|: ||::|||  |||||||:|:  :|||||
Db        181 ISRKTHNRIENMVKNIDPGTVMLLTNYIYFQGRWQYEFDPKQTKEEDFFIEEGKTVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||: |:| : || :|||||||:||: |||| |:||| |||: ||:||| | |::||:|||
Db        241 MFQRGMYDMAYDSQLSCTILEMPYRGNITATFVLPDSGKLRLLEQGLQADIFAKWKSLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              :||||| ||||:: |:::|| || :|:|||||||||||:|: |||||||||||||:|
Db        301 KRVVDVWVPRLHISATYNMKKVLSRLGISKIFEEHGDLTRISSHRSLKVGEAVHKAELRM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              :|:|||||||:|||||||||  :|:: |:|::||   :||::|| :| ||
Db        361 NEKGTEGAAGSGAQTLPMETPRRMKLNAPFLMMIYENLMPSMIFLARIYNP 411


RESULT 3
Q7TMF5_MOUSE
ID   Q7TMF5_MOUSE PRELIMINARY;      PRT;   413 AA.
AC   Q7TMF5;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Visceral adipose-specific SERPIN.
GN   Name=Serpina12;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Swiss Webster;
RA   Hida K., Wada J., Zhang H.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the serpin family.
DR   EMBL; AY326419; AAP88383.1; -; mRNA.
DR   HSSP; P01008; 1ATH.
DR   MGI; MGI:1915304; Serpina12.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR000295; Prot_inh_Lserp2.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   Pfam; PF00079; Serpin; 1.
DR   PRINTS; PR00780; LEUSERPINII.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Serpin.
SQ   SEQUENCE   413 AA;  47674 MW;  EE2B3B08C2DD418F CRC64;
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  Query Match           64.8%;  Score 1380;  DB 2;  Length 413;
  Best Local Similarity  61.3%;  Pred. No. 6.3e-90;
  Matches  253;  Conservative   85;  Mismatches   75;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              |   | | :||| ||||||||:   :|  | :   || |: :  |::||| ||: |||||
Db          1 MTRMLDLGLFLAGLLTVKGLLQDRDAPDMYDSPVRVQEWRGKKDARQLARHNMEFGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ::||  :|  |||||||||||||||| ||||:|||:||::||||::|  :|:|  |||::
Db         61 QRLASNSPRGNIFLSPLSISTAFSMLSLGAQNSTLEEIREGFNFKEMSNRDVHAAFHYLL 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              |:| |:|:| |:::|| ||:||:|:||::||  ||| | |: :|||||:||  || || :
Db        121 HKLNQETEDTKMNLGNALFMDQKLRPQQRFLNLAKNVYDADMVLTNFQDLENTQKDINRY 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||:||| :| |::::|||||||:| |||:|| ||::|||  ||||:||:||  :|||||
Db        181 ISRKTHSRIKNMVKSIDPGTVMILTNYIYFRGRWQYEFDPKQTKEEEFFIEKGKTVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||: |:| : || :|||||||||: |||| |:||| |||| ||:||| | |::||:|||
Db        241 MFQRGLYDMAYDSQLSCTILEIPYRGNITATFVLPDNGKLKLLEQGLQADIFAKWKSLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              :||||| ||:| :: |:::|| || :|:|||||:||||:|: ||||||||||||||||
Db        301 KRVVDVWVPKLRISSTYNMKKVLSRLGISKIFEENGDLTRISSHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIG 413
              ||:| |||||:|||||||||||  :|:|:|:|::||   :||::|| :| :| |
Db        361 DEKGMEGAAGSGAQTLPMETPRHMKLDRPFLMMIYENFMPSMIFLARIYDPSG 413


RESULT 4
Q9CQ32_MOUSE
ID   Q9CQ32_MOUSE PRELIMINARY;      PRT;   413 AA.
AC   Q9CQ32;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched
DE   library, clone:4632419J12 product:hypothetical Serpins containing
DE   protein, full insert sequence (Mus musculus 17 days embryo head cDNA,
DE   RIKEN full-length enriched library, clone:3300001F13
DE   product:hypothetical Serpins containing protein, full insert
DE   sequence).
GN   Name=Serpina12;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
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RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the serpin family.
DR   EMBL; AK014589; BAB29447.1; -; mRNA.
DR   EMBL; AK014346; BAB29287.1; -; mRNA.
DR   HSSP; P01008; 1ATH.
DR   Ensembl; ENSMUSG00000041567; Mus musculus.
DR   MGI; MGI:1915304; Serpina12.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR000295; Prot_inh_Lserp2.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   Pfam; PF00079; Serpin; 1.
DR   PRINTS; PR00780; LEUSERPINII.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Hypothetical protein; Serpin.
SQ   SEQUENCE   413 AA;  47634 MW;  D0AE8E1EE24FD60A CRC64;

  Query Match             64.7%;  Score 1378;  DB 2;  Length 413;
  Best Local Similarity   61.5%;  Pred. No. 8.8e-90;
  Matches  254;  Conservative   83;  Mismatches   76;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              |   | | :||| ||||||||:   :|  | :   || |: :  |::||| ||: |||||
Db          1 MTRMLDLGLFLAGLLTVKGLLQDRDAPDMYDSPVRVQEWRGKKDARQLARHNMEFGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ::||  :|  ||||||||||||||| ||||:|||:||::||||::|   |:|  |||::
Db         61 QRLASNSPQGNIFLSPLSISTAFSMLSLGAQNSTLEEIREGFNFKEMSNWDVHAAFHYLL 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              |:| |:|:| |:::|| ||:||:|:||::||  ||| | |: :|||||:||  || || :
Db        121 HKLNQETEDTKMNLGNALFMDQKLRPQQRFLNLAKNVYDADMVLTNFQDLENTQKDINRY 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              |||||| :| |::::|||||||:| |||:|| ||::|||  ||||:||:||  :|||||
Db        181 ISQKTHSRIKNMVKSIDPGTVMILTNYIYFRGRWQYEFDPKQTKEEEFFIEKGKTVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||: |:| : || :|||||||||: |||| |:||| |||| ||:||| | |::||:|||
Db        241 MFQRGLYDMAYDSQLSCTILEIPYRGNITATFVLPDNGKLKLLEQGLQADIFAKWKSLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              :||||| ||:| :: |:::|| || :|:||||||:||||:|: ||||||||||||||||
Db        301 KRVVDVWVPKLRISSTYNMKKVLSRLGISKIFEENGDLTRISSHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIG 413
              ||:| |||||:|||||||||||  :|:|:|:|::||   :||::|| :| :| |
Db        361 DEKGMEGAAGSGAQTLPMETPRHMKLDRPFLMMIYENFMPSMVFLARIYDPSG 413


RESULT 5
Q6P6M3_MOUSE
ID   Q6P6M3_MOUSE PRELIMINARY;      PRT;   413 AA.
AC   Q6P6M3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Visceral adipose-specific SERPIN.
GN   Name=Serpina12;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Jaw and Limb;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Jaw and Limb;
RG   NIH MGC Project;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the serpin family.
DR   EMBL; BC062143; AAH62143.1; -; mRNA.
DR   HSSP; P01008; 1ATH.
DR   Ensembl; ENSMUSG00000041567; Mus musculus.
DR   MGI; MGI:1915304; Serpina12.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR000295; Prot_inh_Lserp2.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   Pfam; PF00079; Serpin; 1.
DR   PRINTS; PR00780; LEUSERPINII.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW   Serpin.
SQ   SEQUENCE   413 AA;  47630 MW;  CE1940BA2EE35811 CRC64;

  Query Match             64.3%;  Score 1369;  DB 2;  Length 413;
  Best Local Similarity   60.5%;  Pred. No. 3.8e-89;
  Matches  250;  Conservative   87;  Mismatches   76;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              |   | | :| | ||||||||:   :|  | :   || |: :  |::||| ||: |||||
Db          1 MTRMLDLGLFPAGLLTVKGLLQDRDAPDMYDSPVRVQEWRGKKDARQLARHNMEFGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ::||  :|  ||||||||||||||| ||||:|||:||::||||::|   :|:|  |||::
Db         61 QRLASNSPRGNIFLSPLSISTAFSMLSLGAQNSTLEEIREGFNFKEMSNRDVHAAFHYLL 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              |:| |:|:| |:::|| ||:||:|:||::||  ||| | |: :|||||:||  || || :
Db        121 HKLNQETEDTKMNLGNALFMDQKLRPQQRFLNLAKNVYDADMVLTNFQDLENTQKDINRY 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||:||| :| |::::|||||||:| |||:|| ||::|||  ||||:||:||  :|||||
Db        181 ISRKTHSRIKNMVKSIDPGTVMILTNYIYFRGRWQYEFDPKQTKEEEFFIEKGKTVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||: |:| : || :|||||||||: |||| |:||| |||| ||:||| | |::||:|||
Db        241 MFQRGLYDMAYDSQLSCTILEIPYRGNITATFVLPDNGKLKLLEQGLQADIFAKWKSLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              :||||| ||:| :: |:::|| || :|:||||||:||||:|: ||||||||||||||||
Db        301 KRVVDVWVPKLRISSTYNMKKVLSRLGISKIFEENGDLTRISSHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIG 413
              ||:| |||||:|||||||||||  :|:|:|:|::||   :||::|| :| :| |
Db        361 DEKGMEGAAGSGAQTLPMETPRHMKLDRPFVMMIYENFMPSMIFLARVYDPSG 413
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RESULT 6
Q7SYX0_XENLA
ID   Q7SYX0_XENLA PRELIMINARY;      PRT;   432 AA.
AC   Q7SYX0;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Serpina1d-prov protein.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RA   Klein S., Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the serpin family.
DR   EMBL; BC054235; AAH54235.1; -; mRNA.
DR   HSSP; P01008; 1ATH.
DR   GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR   InterPro; IPR000295; Prot_inh_Lserp2.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   Pfam; PF00079; Serpin; 1.
DR   PRINTS; PR00780; LEUSERPINII.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW   Serpin.
SQ   SEQUENCE   432 AA;  48872 MW;  B5B25EC0BAF1033B CRC64;

  Query Match             41.2%;  Score 876.5;  DB 2;  Length 432;
  Best Local Similarity   43.7%;  Pred. No. 5.1e-54;
  Matches  163;  Conservative   88;  Mismatches  119;  Indels    3;  Gaps    2;

Qy         41 QRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQ 100
              : |:  ::|  |    |:  :::|  :|  ||| ||:|||||||| |||:  ||::| :
Db         59 ETMSCHKIAPFNAQFAFEFYRQVAADHPSENIFFSPVSISTAFSMLSLGAKGQTLNQIIE 118

Qy        101 --GFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFY 158
                 |||  :: |:::| || :::| |     :|:|: || ||||  ::  :||||| | ||
Db        119 GLGFNTTEISEEEIHNGFQHLLHMLNDPDSELQLNSGNALFIDNNMKLIQKFLEDVKEFY 178

Qy        159 SAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEF 218
               :|   |:| | : | |||| :: :|||||| :|:::::|   |:::| |||:|| :|:  |
Db        179 ESEAFSTDFHNTKEATKQINSYVEKKTHGKITDLLKDVDERTLLILINYIYFRGKWEKPF 238

Qy        219 DPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEG 278
              :   |::  | :::|::| |||| |:|:| | :|||| ||:::|||: | |::|||||||
Db        239 EEEFTQDGIFHVDENTNVTVPMMRRNGMYNVAFDDKLGCTVVQIPYKGNATSLFILPDEG 298

Qy        279 KLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDL 338
              ||| :|: |:  |   || |   | ||:::|:  ::  || :     ||  :| :  ||
Db        299 KLKQVEEALEKSTIMSWKKLFGYRSVDLTIPKFSVSAELDLVEVFKKFGVKDVFSDLADL 358

Qy        339 TKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEK 398
              | ||  | ||| :|:||| | :||:||| || |  : :||  |  :| ::|:|: || ::
Db        359 TGIAASR-LKVSKALHKAVLSIDEKGTEAAAATAFEIMPMMIPPNIKFNQPFLITIYDQE 417

Qy        399 IPSVLFLGKIVNP 411
               | ||||:| ||
Db        418 TRSTLFLGRITNP 430


RESULT 7
Q66KX6_XENLA
ID   Q66KX6_XENLA PRELIMINARY;      PRT;   431 AA.
AC   Q66KX6;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   MGC85345 protein.
GN   Name=MGC85345;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the serpin family.
DR   EMBL; BC078523; AAH78523.1; -; mRNA.
DR   GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR   InterPro; IPR000295; Prot_inh_Lserp2.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   Pfam; PF00079; Serpin; 1.
DR   PRINTS; PR00780; LEUSERPINII.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Serpin.
SQ   SEQUENCE   431 AA;  48870 MW;  41ADE4EC6BE6ED57 CRC64;

  Query Match             40.2%;  Score 857;  DB 2;  Length 431;
  Best Local Similarity   42.6%;  Pred. No. 1.3e-52;
  Matches  159;  Conservative   91;  Mismatches  121;  Indels    2;  Gaps    1;

Qy         41 QRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQ 100
              : |   ::|  |    | | :|:|  ||  ||||||:||||||:|| |||:  || :| :
Db         57 ESMPCLKIAPYNAHFSFSLYRKIAADNPTENIFLSPVSISTAFAMLSLGARGQTLKQITE 116

Qy        101 G--FNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFY 158
              |  ||  :: |:::|:|| :::| |     :::|: || ||||:  |  :||:|||| ||
Db        117 GLSFNTTEISEEEIHKGFQHLLHMLNDPNSEMQLNSGNALFIDKDFQIIQKFVEDAKQFY 176

Qy        159 SAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEF 218
              || : |:| | | | |||| :  :||:|||  |:  :|  |:::| |||:|| :|:  |
Db        177 EAEPVSTDFHNTEEATKQINSYAEKKTNGKITELLSTVDEKTLLVLINYIYFRGQWEKPF 236

Qy        219 DPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEG 278
              :   | : :| ::|:: | |||| ::|:| | |||:| ||:: :||: | ||:|||||||
Db        237 EKENTVDGEFHVDKDTVVTVPMMHKNGMYNVAYDDQLGCTVVLMPYKGNATALFILPDEG 296

Qy        279 KLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDL 338
              ||: :|: |:       |: :  || |::::|:  :: | || | |: :||: :| :  :|
Db        297 KLRQVEEALETPVVKSWRKIFRRRSVNLTLPKFSISATLDLVKELTKLGVTDVFSDGSNL 356

Qy        339 TKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEK 398
              : |     |:| :||||| | :|| ||| |  || : :||  |  :: :||:|::|| ::
Db        357 SGITEAPPLRVSKAVHKALLSIDETGTEAAGVTGMELMPMMVPSRIEFNKPFLIIIYGQE 416

Qy        399 IPSVLFLGKIVNP 411
                |  |:|:|:||
Db        417 TRSNYFMGRIMNP 429


RESULT 8
Q9YIB8_XENLA
ID   Q9YIB8_XENLA PRELIMINARY;      PRT;   433 AA.
AC   Q9YIB8;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Alpha-1-antiproteinase.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
RA   Yoshida K., Suzuki Y., Sinohara H.;
RT   "Cloning and comparative sequence analysis of Xenopus laevis alpha1-
RT   antiproteinase.";
RL   J. Biochem. Mol. Biol. Biophys. 3:59-63(1999).
CC   -!- SIMILARITY: Belongs to the serpin family.
DR   EMBL; AB014091; BAA36581.1; -; mRNA.
DR   HSSP; P01009; 1QMB.
DR   GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR   InterPro; IPR000295; Prot_inh_Lserp2.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   Pfam; PF00079; Serpin; 1.
DR   PRINTS; PR00780; LEUSERPINII.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW   Serpin.
SQ   SEQUENCE   433 AA;  48909 MW;  4E37C65317BCF2AC CRC64;

  Query Match             40.2%;  Score 857;  DB 2;  Length 433;
  Best Local Similarity   42.6%;  Pred. No. 1.3e-52;
  Matches  159;  Conservative   87;  Mismatches  125;  Indels    2;  Gaps    1;

Qy         41 QRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQ 100
              : |:  ::|  |    |:  :::|  :|  ||| ||:||||: ::| |||:  ||::| :
Db         59 EHMSCHKIAPFNAQFAFEFYRQVAVDHPSENIFFSPVSISTSLALLSLGAKGQTLNQIVE 118

Qy        101 G--FNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFY 158
              |  ||  :: |:|:|:|| :::| |     :|:|: || |||   |:  :||||| || |
Db        119 GLDFNTTEISEEDIHKGFQHLLHMLNDPDSELQLNSGNALFIRNNLKLIQKFLEDVKNIY 178

Qy        159 SAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEF 218
              :|   |:||| | |:|||| :: :|||||| :|: ::|  | ::| |||:|| :|   |
Db        179 GSEAFSTDFQNAEEAKKQINSYVEKKTHGKITDLLSSVDESTALILINYIYFRGKWDKPF 238

Qy        219 DPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEG 278
              |  :|::  |::::|::| |||| |:|:|  | :|  || ||:::|||: | :|:|||||||
Db        239 DEELTQDGIFYVDENTNVTVPMMRRTGMYNVAFDRKLGCTVVQIPYKGNASALFILPDEG 298

Qy        279 KLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDL 338
              ||| :|  |:  |   || |    : | :|:|:  ::   || :    :||: :| :  ||
Db        299 KLKQVEAALERPTIMSWKKLFRYQSVRLSIPKFSISAELDLIEVFKKLGVTDVFSDEADL 358

Qy        339 TKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEK 398
              | |      ||| :||||| | :||:||| || |  : :||  |  :: ::|:|| ||  :
Db        359 TGIVEEAKLKVSKAVHKAVLSIDEKGTEAAARTAFEIMPMMLPPNIQYNRPFLLTIYDME 418

Qy        399 IPSVLFLGKIVNP 411
                  ||||:| ||
Db        419 TKHTLFLGRIANP 431


RESULT 9
Q5M911_XENTR
ID   Q5M911_XENTR PRELIMINARY;      PRT;   436 AA.
AC   Q5M911;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   LOC496632 protein (Fragment).
GN   Name=LOC496632;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole body;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole body;
RA   Klein S., Gerhard D.S.;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the serpin family.
DR   EMBL; BC087750; AAH87750.1; -; mRNA.
DR   GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR   InterPro; IPR000295; Prot_inh_Lserp2.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   Pfam; PF00079; Serpin; 1.
DR   PRINTS; PR00780; LEUSERPINII.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW   Serpin.
FT   NON_TER       1      1
SQ   SEQUENCE   436 AA;  49692 MW;  07EB4D2A7446A34B CRC64;

  Query Match             39.5%;  Score 841;  DB 2;  Length 436;
  Best Local Similarity   42.1%;  Pred. No. 1.8e-51;
  Matches  157;  Conservative   94;  Mismatches  120;  Indels    2;  Gaps    1;

Qy         41 QRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQ 100
              :|    ::|   | : || | :::|   :|  |||:||:|||| |:|| ||| : :||::| :
Db         62 ESMPCLKIAPYNANPGFSLYRQIAADHPTENIPISPVSISTVPAMLSLGARSNTLNQIIE 121

Qy        101 G--FNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFY 158
              |  ||  :: |:::|:|| :::| |       ::|: || |||| ||  :||:||:| ||
Db        122 GLKFNRSELTEEEMHKGFQHLLHMLNDPNSKVQLNSGNALFIDKDLQLIQKFVEDSKQFY 181

Qy        159 SAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEF 218
               |||  |:| | | | |||| :   || ||| :|: ::|  |:::| |||:|   |:  |
Db        182 EAETFSTDFHNTEEATKQINTYAENKTKGKITDLLSSVDEKTILVLINYIYFYGEWEKHF 241

Qy        219 DPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEG 278
              :  ||:  | :::|::| |||| |:|:| | :|:|| ||:::||: | ||:|||||||
Db        242 EKEWTKDGIFHVDENTNVTVPMMHRNGMYNVAFDEKLGCTVVQIPYKGNATALFILPDEG 301

Qy        279 KLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDL 338
              ||: :|: |:       || |  :| | :::|:| :: | || | || :||: :| :: ||
Db        302 KLRQVEEALEKAVVKSWKKLFRKRFVHLTLPKLSISATTDLVKELSKLGVTDVFSDNSDL 361

Qy        339 TKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEK 398
              : |      ||| :|||| : :|| ||| |  |  : :|   |  :: ::|::|:||
Db        362 SGIVDVTPLKVSKAVHKVLVSIDETGTEAAGVTVMEIVPTMLPPRIEYNRPFVLMIYEPT 421

Qy        399 IPSVLFLGKIVNP 411
              : : ||:|:::||
Db        422 LRANLFMGRVMNP 434


RESULT 10
Q8JIA6_SPHPU
ID   Q8JIA6_SPHPU PRELIMINARY;      PRT;   426 AA.
AC   Q8JIA6;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Alpha-1-antitrypsin (Fragment).
OS   Sphenodon punctatus (Hatteria) (Tuatara).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Sphenodontia; Sphenodontidae; Sphenodon.
OX   NCBI_TaxID=8508;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Metcalf V.J., Brennan S.O., George P.M., Chambers G.K.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the serpin family.
DR   EMBL; AF375974; AAM46107.1; -; mRNA.
DR   HSSP; P01009; 1EZX.
DR   GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   Pfam; PF00079; Serpin; 1.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW   Serpin.
FT   NON_TER       1      1
SQ   SEQUENCE   426 AA;  48318 MW;  6D75C8737FE70950 CRC64;

  Query Match             38.8%;  Score 827;  DB 2;  Length 426;
  Best Local Similarity   39.6%;  Pred. No. 1.7e-50;
  Matches  170;  Conservative   93;  Mismatches  142;  Indels   24;  Gaps    6;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPR---------NYKALSEVQGW---KQRMAAKEL 48
              | ||| | : ||           ::|          ' ::|    |        : |   ::
Db          1 MTPTLHLCLLLAWFCAF------AYSHHHPDHQHDHDDHKDKQETHAGAPPSKNMTCHKI 54

Qy         49 ARQNMDLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQG--FNFRK 106
              | | |  |:  |::|    | :|:| ||:||||||:|| |||: :|  :| :|  || :
Db         55 APSNADFAFRFYKQIAAEAPAKNVFFSPVSISTAFAMLTLGAKSTTQSQIYEGLAFNLTE 114

Qy        107 MPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTN 166
              : |:::|||| : |   :  ::: |::|| ||||::|:|  |||:| |:||::|   :|
Db        115 IEEQEIHEGFRHFIQMFSLSDREILLNMGNALFIDEKLKPIPKFLDDIKSFYASEGFSSN 174

Qy        167 FQNLEMAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEE 226
              | :   |:|||||:| :|| |:| :|::|: | |||:| |||  :| |:| |:   |:||
Db        175 FTDSAEAEKQINDYIKKKTKGEIVDLVKNLGPDTVMVLVNYILLKAYWEHPFNYEATREE 234

Qy        227 DFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI--LEIPYQKNITAIFILPDEGKLKHLE 284
              |||::  :|||| ||    |  :| |||| :  :::| |:|: | |||||||:| :|
Db        235 DFFVDGKTSVKVDMMNPDSRYNSLHDKKLSCLVQWVDLPLQRNVAATFILPDEGKMKQVE 294

Qy        285 KGLQVDTFSRWKTLL--SRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIA 342
              | |:  :| :  |   | : :|:||  ::||:|:|:    :||:::|    ||: |
Db        295 DALSVEVLTRLEKSLRKERSRIHLSIPRFSISGTYDVKEIFRRMGVTEVFTNQADLSGIT 354

Qy        343 PHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSV 402
              |||  |||:| | : | ||| :| |  : :||  | |||::|:|:  | :   ||
Db        355 GSPELKVSRAVHRAHLNVHENGTEASATTVIELVPMSLPPVVKLNRPFLFSIVDKTAHSV 414

Qy        403 LFLGKIVNP 411
              ||:||:|||
Db        415 LFMGKVVNP 423


RESULT 11
A1AT_CERAE
ID   A1AT_CERAE     STANDARD;      PRT;   396 AA.
AC   O00394;
DT   13-SEP-2005 (Rel. 48, Created)
DT   13-SEP-2005 (Rel. 48, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-
DE   antiproteinase) (Fragment).
GN   Name=SERPINA1;
OS   Cercopithecus aethiops (Green monkey) (Grivet).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Cercopithecus.
OX   NCBI_TaxID=9534;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Kidney;
RA   Yoshida K., Suzuki Y., Yamamoto K., Watanabe M., Sinohara H.;
RT   "Cloning and sequencing of complementary DNAs encoding alpha-2-HS
RT   glycoprotein, alpha-1-antitrypsin, and beta-actin from african green
RT   monkey, Cercopithecus aethiops.";
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RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Inhibitor of serine proteases. Its primary target is
CC       elastase, but it also has a moderate affinity for plasmin and
CC       thrombin (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- TISSUE SPECIFICITY: Plasma.
CC   -!- DOMAIN: The reactive center loop (RCL) extends out from the body
CC       of the protein and directs binding to the target protease. The
CC       protease cleaves the serpin at the reactive site within the RCL,
CC       establishing a covalent linkage between the carboxyl group of the
CC       serpin reactive site and the serine hydroxyl of the protease. The
CC       resulting inactive serpin-protease complex is highly stable (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the serpin family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AB004044; BAA20264.1; -; mRNA.
DR   HSSP; P01009; 1EZX.
DR   SMR; O00394; 25-396.
DR   GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; NAS.
DR   GO; GO:0030162; P:regulation of proteolysis and peptidolysis; NAS.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   PANTHER; PTHR11461; Prot_inh_serpin; 1.
DR   Pfam; PF00079; Serpin; 1.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Acute phase; Glycoprotein; Protease inhibitor;
KW   Serine protease inhibitor; Serpin; Signal.
FT   SIGNAL       <1      2       Potential.
FT   CHAIN         3    396       Alpha-1-antitrypsin.
FT   REGION      351    370       RCL.
FT   SITE        360    361       Reactive bond (By similarity).
FT   CARBOHYD     48     48       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     85     85       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    123    123       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    249    249       N-linked (GlcNAc. . .) (Potential).
FT   NON_TER       1      1
SQ   SEQUENCE   396 AA;  44587 MW;  1042EABFAA0A2825 CRC64;

  Query Match             37.2%;  Score 792;  DB 1;  Length 396;
  Best Local Similarity   42.1%;  Pred. No. 4.8e-48;
  Matches  153;  Conservative   81;  Mismatches  127;  Indels    2;  Gaps    1;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
              :  | | ::|| :    ||| ||:||:|||:|| || :  |  || :| ||   ::||
Db         34 EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHSEILEGLNFNLTEIPEAQ 93

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
              :|||| ::| | :    |:|: || ||::: ::   ||||| |  | :|    ||:: |
Db         94 IHEGFQELLHTLNKPDSQLQLTTGNGLFLNKSVKVVDKFLEDVKKLYHSEAFSVNFEDTE 153

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
              |:|||::: : | ||| :|:: :|  ||  | |||||: :|:  |:   |||||| ::
Db        154 EAKKQINNYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVEATKEEDFHVD 213

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
              : ::|||||| | |:: : : :|||  :| : |  | |||| |||||||:|||  |  |
Db        214 QATTVKVPMMRRLGMFNIYHCEKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 273

Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
              :::    :||  :: :|:| :|||:|||  | ::|::|:|    ||: :    ||: :
Db        274 ITKFLENENRRSANLHLPKLAITGTYDLKTVLGHLGITKVFSNGADLSGVTEDAPLKLSK 333

Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              ||||| | :||:||| |     : :||  |  || :||:: |:  :   | ||:||:|||
Db        334 AVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNP 393

Qy        412 IGK 414
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                |
Db        394 TQK 396


RESULT 12
A1AT_PONPY
ID   A1AT_PONPY     STANDARD;      PRT;   418 AA.
AC   Q5RCW5; Q5NVR9; Q5RF76;
DT   13-SEP-2005 (Rel. 48, Created)
DT   13-SEP-2005 (Rel. 48, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-
DE   antiproteinase).
GN   Name=SERPINA1;
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Heart, Kidney, and Liver;
RG   The German cDNA consortium;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Inhibitor of serine proteases. Its primary target is
CC       elastase, but it also has a moderate affinity for plasmin and
CC       thrombin (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- TISSUE SPECIFICITY: Plasma.
CC   -!- DOMAIN: The reactive center loop (RCL) extends out from the body
CC       of the protein and directs binding to the target protease. The
CC       protease cleaves the serpin at the reactive site within the RCL,
CC       establishing a covalent linkage between the carboxyl group of the
CC       serpin reactive site and the serine hydroxyl of the protease. The
CC       resulting inactive serpin-protease complex is highly stable (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the serpin family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; CR857285; CAH89581.1; -; mRNA.
DR   EMBL; CR858153; CAH90392.1; -; mRNA.
DR   EMBL; CR925936; CAI29594.1; -; mRNA.
DR   SMR; Q5RCW5; 47-418.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   PANTHER; PTHR11461; Prot_inh_serpin; 1.
DR   Pfam; PF00079; Serpin; 1.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Acute phase; Glycoprotein; Protease inhibitor;
KW   Serine protease inhibitor; Serpin; Signal.
FT   SIGNAL        1     24       Potential.
FT   CHAIN        25    418       Alpha-1-antitrypsin.
FT   REGION      373    392       RCL.
FT   SITE        382    383       Reactive bond (By similarity).
FT   CARBOHYD     70     70       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    107    107       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    271    271       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT    289    289       N -> D (in Ref. 1; CAH89581).
FT   CONFLICT    305    305       R -> RS (in Ref. 1; CAH89581/CAI29594).
FT   CONFLICT    332    332       I -> T (in Ref. 1; CAH89581).
FT   CONFLICT    396    404       FLMIEQNTK -> CLISVFQNA (in Ref. 1;
FT                                CAI29594).
SQ   SEQUENCE   418 AA;  46861 MW;  BF93D2080AEDBE56 CRC64;

  Query Match             37.1%;  Score 790;  DB 1;  Length 418;
  Best Local Similarity   42.7%;  Pred. No. 7.2e-48;
  Matches  155;  Conservative   76;  Mismatches  130;  Indels    2;  Gaps    1;
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Qy          54 DLGPKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQG--FNFRKMPEKD 111
               :  | | ::||  :   ||| ||:||:|||:|| || :  |  || :|  ||  ::||
Db          56 EPAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHSEILEGLHFNLTEIPEAQ 115

Qy         112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
               :|||| ::  | |    |:|: || ||::: |:  ||||| |  | ::    || : |
Db         116 VHEGFQELLRTLNQPDSQLQLTTGNGLFLNESLKLVDKFLEDVKKLYHSDAFTVNFGDTE 175

Qy         172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
               |:|||||:: : | ||| :|:: :|  ||  | |||||: :|:  |:   |||||| ::
Db         176 EAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTKEEDFHVD 235

Qy         232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
               : ::|||||| | |:: : | :|||  :| : |  | |||| |||||||:|||  |  |
Db         236 EVTTVKVPMMRRLGMFNIHYCEKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 295

Qy         292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
                :::    :||   : :|:| :|||:|||: |  :|::|:|    ||: :     ||: :
Db         296 ITKFLENENRRSASLHLPKLSITGTYDLKRVLGQLGITKVFSNGADLSGVTEEAPLKLSK 355

Qy         352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
               ||||| | :||:||| |     : :||  |  || :||:: |:  :   | ||:||:|||
Db         356 AVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFVGKVVNP 415

Qy         412 IGK 414
                |
Db         416 TQK 418


RESULT 13
A1AT_PAPAN
ID   A1AT_PAPAN     STANDARD;      PRT;   409 AA.
AC   P01010;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-
DE   antiproteinase) (AAT) (Fragment).
GN   Name=SERPINA1; Synonyms=PI;
OS   Papio anubis (Olive baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Papio.
OX   NCBI_TaxID=9555;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=82082539; PubMed=7031661;
RA   Kurachi K., Chandra T., Friezner Degen S.J., White T.T.,
RA   Marchioro T.L., Woo S.L.C., Davie E.W.;
RT   "Cloning and sequence of cDNA coding for alpha 1-antitrypsin.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:6826-6830(1981).
CC   -!- FUNCTION: Inhibitor of serine proteases. Its primary target is
CC       elastase, but it also has a moderate affinity for plasmin and
CC       thrombin.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Plasma.
CC   -!- DOMAIN: The reactive center loop (RCL) extends out from the body
CC       of the protein and directs binding to the target protease. The
CC       protease cleaves the serpin at the reactive site within the RCL,
CC       establishing a covalent linkage between the carboxyl group of the
CC       serpin reactive site and the serine hydroxyl of the protease. The
CC       resulting inactive serpin-protease complex is highly stable (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the serpin family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; J00321; AAA35377.1; -; mRNA.
DR   HSSP; P01009; 1EZX.
DR   SMR; P01010; 38-409.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   PANTHER; PTHR11461; Prot_Inh_serpin; 1.
DR   Pfam; PF00079; Serpin; 1.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Acute phase; Glycoprotein; Protease inhibitor;
KW   Serine protease inhibitor; Serpin; Signal.
FT   SIGNAL       <1     15
FT   CHAIN         16    409       Alpha-1-antitrypsin.
FT   REGION       364    383       RCL.
FT   SITE         373    374       Reactive bond.
FT   CARBOHYD      61     61       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD      98     98       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     136    136       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     262    262       N-linked (GlcNAc. . .) (Potential).
FT   NON_TER        1      1
SQ   SEQUENCE   409 AA;  45694 MW;  E19B0B7450FDBA9B CRC64;

  Query Match             36.9%;  Score 787;  DB 1;  Length 409;
  Best Local Similarity   41.9%;  Pred. No. 1.1e-47;
  Matches  152;  Conservative   82;  Mismatches  127;  Indels    2;  Gaps    1;

Qy          54 DLGPKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
               :  | | ::||  :   ||| ||:||:|||:|| || :  |  || :| ||   ::||
Db          47 EPAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHSEILEGLNFNLTEIPEAQ 106

Qy         112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
               :|||| ::  | :    |:|: || ||::: |:   ||||| || | :|    ||:: |
Db         107 VHEGFQELLRTLNKPDSQLQLTTGNGLFLNKSLKVVDKFLEDVKNLYHSEAFSVNFEDTE 166

Qy         172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
               |:||||::: : | ||: :|:: :|  ||  | |||||: :|:  |:   |:|||| ::
Db         167 EAKKQINNYVEKGTQGKVVDLVKELDRDTVFALVNYIFFKGKWERPFEVEATEEEDFHVD 226

Qy         232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
               : ::|||||| | |:: : : :|||  :| : |  | |||| |||||||:|||  |  |
Db         227 QATTVKVPMMRRLGMFNIYHCEKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 286

Qy         292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
                :::    :||  :: :|:| :|||:|||  | ::|::|:|    ||: :     ||: :
Db         287 ITKFLENENRRSANLHLPKLAITGTYDLKTVLGHLGITKVFSNGADLSGVTEDAPLKLSK 346

Qy         352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
               ||||| | :||:||| |     : :||  |  || :||:: |:  :   | ||:||:|||
Db         347 AVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFIGKVVNP 406

Qy         412 IGK 414
                |
Db         407 TQK 409


RESULT 14
Q28665_RABIT
ID   Q28665_RABIT PRELIMINARY;      PRT;   413 AA.
AC   Q28665;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Alpha-1-antiproteinase E precursor.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC   Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=95251597; PubMed=7733871;
RA   Saito A., Shinohara H.;
RT   "Rabbit alpha-1-antiproteinase E: a novel recombinant serpin which
RT   does not inhibit proteinases.";
RL   Biochem. J. 307:369-375(1995).
CC   -!- SIMILARITY: Belongs to the serpin family.
```

```
DR   EMBL; D17725; BAA04579.1; -; mRNA.
DR   PIR; S54981; S54981.
DR   HSSP; P01009; 1QMB.
DR   GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   Pfam; PF00079; Serpin; 1.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Serpin; Signal.
FT   SIGNAL       1     23       Potential.
FT   CHAIN       24    413       alpha-1-antiproteinase E.
SQ   SEQUENCE   413 AA;  45684 MW;  C0E86D60916639E2 CRC64;

  Query Match             36.9%;  Score 785.5;  DB 2;  Length 413;
  Best Local Similarity   37.5%;  Pred. No. 1.5e-47;
  Matches  155;  Conservative   98;  Mismatches  155;  Indels    5;  Gaps    2;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              | |::  |:   :||   | | | |     :  :     :   |  :|   :    |
Db          1 MPPSVSRAL---LLLAGLGCLLPGFLADEAQETAVSSHEQDHPACHRIAPSLAEFALSLY 57

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQG--FNFRKMPEKDLHEGFHY 118
              :::|  :   ||| ||:||: ||:|| |||:  |  :: :|  ||  :  |  :|:|| :
Db         58 REVAHESNTTNIFFSPVSIALAFAMLSLGAKGDTHTQVLEGLKFNLTETAEAQIHDGFRH 117

Qy        119 IIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQIN 178
              ::| : :   :|:|: || | : : |: | |||||||  | :|  | :|:: | |: :||
Db        118 LLHTVNRPDSELQLAAGNALVVHENLKLQHKFLEDAKNLYQSEAFLVDFRDPEQAKTKIN 177

Qy        179 DFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKV 238
               : : | ||| :|:: :|  |:: | ||:||: :|:  |:|  |||||| ::  ::|:|
Db        178 SHVEKGTRGKIVDLVQELDARTLLALVNYVFFKGKWEKPFEPENTKEEDFHVDATTTVRV 237

Qy        239 PMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTL 298
              ||| | |:| : :   |: |:| : |: | ||:|:|||||||:|||  |  :  :::
Db        238 PMMSRLGMYVMFHCSTLASTVLRMDYKGNATALFLLPDEGKLQHLEDTLTTELIAKFLAK 297

Qy        299 LSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAEL 358
              | | | |  |:| ::||:|||  |  :|::::|  : ||: |     ||| :|:||| |
Db        298 SSLRSVTVRFPKLSISGTYDLKPLLGKLGITQVFSNNADLSGITEQEPLKVSQALHKAVL 357

Qy        359 KMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              :|||||| |  :  : :|   |  : :|:|:| :||| :| | ||:||:|:|
Db        358 TIDERGTEAAGASFVELIPESVPDSITLDRPFLFVIYSHEIKSPLFVGKVVDP 410


RESULT 15
A1AT_RAT
ID   A1AT_RAT       STANDARD;      PRT;   411 AA.
AC   P17475; Q6AYZ5;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Alpha-1-antiproteinase precursor (Alpha-1-antitrypsin) (Alpha-1-
DE   proteinase inhibitor).
GN   Name=Serpina1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   STRAIN=Wistar; TISSUE=Liver;
RX   MEDLINE=91035351; PubMed=2229024;
RA   Misumi Y., Sohda M., Ohkubo K., Takami N., Oda K., Ikehara Y.;
RT   "Molecular cloning and sequencing of the cDNA of rat alpha 1-protease
RT   inhibitor and its expression in COS-1 cells.";
RL   J. Biochem. 108:230-234(1990).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Testis;
RG   NIH - Mammalian Gene Collection (MGC) project;
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 4-411, PROTEIN SEQUENCE OF 25-57, AND
RP   TISSUE SPECIFICITY.
RC   TISSUE=Liver;
RX   MEDLINE=90148955; PubMed=2302382;
RA   Chao S., Chai K.X., Chao L., Chao J.;
RT   "Molecular cloning and primary structure of rat alpha 1-antitrypsin.";
RL   Biochemistry 29:323-329(1990).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 188-389.
RC   TISSUE=Liver;
RA   Flink I.L., Bailey T., Morkin E.;
RL   Submitted (AUG-1989) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Inhibitor of serine proteases. The primary target is
CC       elastase, but also has a moderate affinity for plasmin and
CC       thrombin.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Plasma.
CC   -!- DOMAIN: The reactive center loop (RCL) extends out from the body
CC       of the protein and directs binding to the target protease. The
CC       protease cleaves the serpin at the reactive site within the RCL,
CC       establishing a covalent linkage between the carboxyl group of the
CC       serpin reactive site and the serine hydroxyl of the protease. The
CC       resulting inactive serpin-protease complex is highly stable (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the serpin family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; D00675; BAA00579.1; -; mRNA.
DR   EMBL; BC078824; AAH78824.1; -; mRNA.
DR   EMBL; M32247; AAA40788.1; -; mRNA.
DR   EMBL; X16273; CAA34349.1; -; mRNA.
DR   PIR; A33892; ITRT.
DR   HSSP; P01009; 1QMB.
DR   SMR; P17475; 39-411.
DR   Ensembl; ENSRNOG00000032669; Rattus norvegicus.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   PANTHER; PTHR11461; Prot_inh_serpin; 1.
DR   Pfam; PF00079; Serpin; 1.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Acute phase; Direct protein sequencing; Glycoprotein;
KW   Protease inhibitor; Serine protease inhibitor; Serpin; Signal.
FT   SIGNAL       1     24
FT   CHAIN       25    411       Alpha-1-antiproteinase.
FT   REGION     367    386       RCL.
FT   SITE       376    377       Reactive bond.
FT   CARBOHYD    64     64       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   101    101       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   265    265       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT    14     14       A -> G (in Ref. 1 and 2; AAH78824).
FT   CONFLICT    84     84       L -> V (in Ref. 1).
FT   CONFLICT   247    247       M -> I (in Ref. 4).
FT   CONFLICT   248    248       H -> Y (in Ref. 1).
FT   CONFLICT   318    318       K -> N (in Ref. 1).
FT   CONFLICT   322    322       S -> D (in Ref. 4).
SQ   SEQUENCE   411 AA;  46136 MW;  B4245CFE21C5C761 CRC64;

  Query Match             36.9%;  Score 785;  DB 1;  Length 411;
  Best Local Similarity   38.8%;  Pred. No. 1.6e-47;
  Matches  161;  Conservative   94;  Mismatches  150;  Indels   10;  Gaps    5;

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Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQG--FNFRKMPEKDLHEGFHY 118
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Db          57 RELVHQSNTSNIFFSPMSITTAFAMLSLGSKGDTRKQILEGLEFNLTQIPEADIHKAFHH 116

Qy         119 IIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQIN 178
                ::  | :   :|:|: || ||::: |:   ||||: || | :|    || : | |:| ||
Db         117 LLQTLNRPDSELQLNTGNGLFVNKNLKLVEKFLEEVKNNYHSEAFSVNFADSEEAKKVIN 176

Qy         179 DFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKV 238
                |:: : | ||| :|:: :|  ||  | |||||: :||  |:|  |:: || ::|:::|||
Db         177 DYVEKGTQGKIVDLMKQLDEDTVFALVNYIFFKGKWKRPFNPEHTRDADFHVDKSTTVKV 236

Qy         239 PMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTL 298
                ||| | |:: : |   ||  :| : |  | ||||:|||:||::|||: |  |  ||:  |
Db         237 PMMNRLGMFDMHYCSTLSSWVLMMDYLGNATAIFLLPDDGKMQHLEQTLTKDLISRF--L 294

Qy         299 LSR--RVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKA 356
                |:|  |   :  |:| ::||::||  || :|::::|    ||: |     ||: :|||||
Db         295 LNRQTRSAILYFPKLSISGTYNLKTLLSSLGITRVFNNDADLSGITEDAPLKLSQAVHKA 354

Qy         357 ELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
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Db         355 VLTLDERGTEAAGATVVEAVPMSLPPQVKFDHPFIFMIVESETQSPLFVGKVIDP 409
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Search completed: March 31, 2006, 09:50:05
Job time : 235 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 09:51:09 ; Search time 167 Seconds
(without alignments)
1035.816 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 2130
Sequence: 1 MNPTLGLAIFLAVLLTVKGL.....YSEKIPSVLFLGKIVNPIGK 414

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2130	100.0	414	3	US-09-755-665-14	Sequence 14, Appl
2	2130	100.0	414	3	US-09-755-665-55	Sequence 55, Appl
3	2130	100.0	414	3	US-09-755-665-56	Sequence 56, Appl
4	2130	100.0	414	4	US-10-168-425-12	Sequence 12, Appl
5	2130	100.0	414	4	US-10-629-248-14	Sequence 14, Appl
6	2130	100.0	414	4	US-10-629-248-55	Sequence 55, Appl
7	2130	100.0	414	4	US-10-629-248-56	Sequence 56, Appl
8	2130	100.0	415	4	US-10-012-542-134	Sequence 134, App
9	2130	100.0	415	4	US-10-115-123-134	Sequence 134, App
10	2130	100.0	415	4	US-10-800-834-134	Sequence 134, App
11	2114	99.2	431	4	US-10-276-774-2202	Sequence 2202, Ap
12	1798	84.4	361	3	US-09-755-665-57	Sequence 57, Appl
13	1798	84.4	361	4	US-10-629-248-57	Sequence 57, Appl
14	842	39.5	377	4	US-10-037-417-66	Sequence 66, Appl
15	840	39.4	371	4	US-10-023-634-87	Sequence 87, Appl
16	837	39.3	377	3	US-09-823-187-31	Sequence 31, Appl
17	786	36.9	418	5	US-10-741-600-1216	Sequence 1216, Ap
18	786	36.9	418	5	US-10-741-600-1217	Sequence 1217, Ap
19	786	36.9	418	5	US-10-741-600-1218	Sequence 1218, Ap
20	786	36.9	418	5	US-10-741-600-1219	Sequence 1219, Ap
21	786	36.9	418	5	US-10-741-600-1220	Sequence 1220, Ap
22	786	36.9	418	5	US-10-741-600-1221	Sequence 1221, Ap
23	786	36.9	418	5	US-10-741-600-1222	Sequence 1222, Ap
24	785	36.9	363	3	US-09-755-665-58	Sequence 58, Appl
25	785	36.9	363	4	US-10-629-248-58	Sequence 58, Appl
26	785	36.9	394	3	US-09-993-180-6	Sequence 6, Appli
27	785	36.9	394	4	US-10-025-514-2	Sequence 2, Appli
28	785	36.9	394	4	US-10-365-738-1	Sequence 1, Appli
29	785	36.9	394	6	US-11-077-276-2	Sequence 2, Appli
30	785	36.9	395	5	US-10-914-863-2	Sequence 2, Appli
31	785	36.9	418	4	US-10-097-340-286	Sequence 286, App
32	785	36.9	418	4	US-10-411-037-22	Sequence 22, Appl
33	785	36.9	418	4	US-10-411-026-22	Sequence 22, Appl
34	785	36.9	418	4	US-10-410-962-22	Sequence 22, Appl
35	785	36.9	418	4	US-10-411-049-22	Sequence 22, Appl
36	785	36.9	418	4	US-10-408-765A-2304	Sequence 2304, Ap
37	785	36.9	418	4	US-10-410-930-22	Sequence 22, Appl
38	785	36.9	418	4	US-10-410-997-22	Sequence 22, Appl
39	785	36.9	418	4	US-10-411-012-22	Sequence 22, Appl
40	785	36.9	418	4	US-10-287-994-22	Sequence 22, Appl
41	785	36.9	418	4	US-10-410-913-22	Sequence 22, Appl
42	785	36.9	418	5	US-10-410-980-22	Sequence 22, Appl
43	785	36.9	418	5	US-10-971-461-15	Sequence 15, Appl
44	785	36.9	418	5	US-10-410-897-22	Sequence 22, Appl
45	785	36.9	418	5	US-10-492-261-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-09-755-665-14
; Sequence 14, Application US/09755665
; Patent No. US20020107186A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Taillon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-14

Query Match 100.0%; Score 2130; DB 3; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.1e-178;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
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Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
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Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 2
US-09-755-665-55
; Sequence 55, Application US/09755665
; Patent No. US20020107186A1
; GENERAL INFORMATION:
;  APPLICANT: Prayaga, Sudhirdas K.
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Taillon, Bruce E.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  MacDougall, John
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-631
;  CURRENT APPLICATION NUMBER: US/09/755,665
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
;   LENGTH: 414
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-755-665-55

  Query Match             100.0%;  Score 2130;  DB 3;  Length 414;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-178;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
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Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
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Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
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Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
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Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
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RESULT 3
US-09-755-665-56
; Sequence 56, Application US/09755665
; Patent No. US20020107186A1
; GENERAL INFORMATION:
;  APPLICANT: Prayaga, Sudhirdas K.
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Taillon, Bruce E.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  MacDougall, John
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-631
;  CURRENT APPLICATION NUMBER: US/09/755,665
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
;   LENGTH: 414
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-755-665-56

  Query Match             100.0%;  Score 2130;  DB 3;  Length 414;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-178;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
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Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
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Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
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Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 4
US-10-168-425-12
; Sequence 12, Application US/10168425
; Publication No. US20030124706A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  YANG, Junming
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  BURFORD, Neil
;  APPLICANT:  AU-YOUNG, Janice
;  APPLICANT:  LU, Dyung Aina M.
;  APPLICANT:  REDDY, Roopa
;  APPLICANT:  YUE, Henry
;  APPLICANT:  NGUYEN, Danniel B.
;  APPLICANT:  TANG, Y. Tom
;  APPLICANT:  YAO, Monique G.
;  APPLICANT:  LAL, Preeti
;  TITLE OF INVENTION: PROTEASES
;  FILE REFERENCE: PI-0003 PCT
;  CURRENT APPLICATION NUMBER: US/10/168,425
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/172,055; 60/177,334; 60/178,884; 60/179,903
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;  PRIOR FILING DATE: 1999-12-23; 2000-01-21; 2000-01-28; 2000-02-02
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PERL Program
; SEQ ID NO 12
;   LENGTH: 414
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030124706A1 7257324CD1
US-10-168-425-12

  Query Match           100.0%;  Score 2130;  DB 4;  Length 414;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-178;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
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Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
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Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
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Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
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Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 5
US-10-629-248-14
; Sequence 14, Application US/10629248
; Publication No. US20040116671A1
; GENERAL INFORMATION:
;  APPLICANT: Prayaga, Sudhirdas K.
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Taillon, Bruce E.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  MacDougall, John
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-631
;  CURRENT APPLICATION NUMBER: US/10/629,248
;  CURRENT FILING DATE:  2003-07-28
;  PRIOR APPLICATION NUMBER: US/09/755,665
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 414
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-629-248-14

  Query Match           100.0%;  Score 2130;  DB 4;  Length 414;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-178;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 6
US-10-629-248-55
; Sequence 55, Application US/10629248
; Publication No. US20040116671A1
; GENERAL INFORMATION:
;  APPLICANT: Prayaga, Sudhirdas K.
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Taillon, Bruce E.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  MacDougall, John
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-631
;  CURRENT APPLICATION NUMBER: US/10/629,248
;  CURRENT FILING DATE:  2003-07-28
;  PRIOR APPLICATION NUMBER: US/09/755,665
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
;   LENGTH: 414
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-629-248-55

  Query Match           100.0%;  Score 2130;  DB 4;  Length 414;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-178;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 7
US-10-629-248-56
; Sequence 56, Application US/10629248
; Publication No. US20040116671A1
; GENERAL INFORMATION:
;  APPLICANT: Prayaga, Sudhirdas K.
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Taillon, Bruce E.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  MacDougall, John
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-631
;  CURRENT APPLICATION NUMBER: US/10/629,248
;  CURRENT FILING DATE:  2003-07-28
;  PRIOR APPLICATION NUMBER: US/09/755,665
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
;   LENGTH: 414
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-629-248-56

  Query Match             100.0%;  Score 2130;  DB 4;  Length 414;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-178;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 8
US-10-012-542-134
; Sequence 134, Application US/10012542
; Publication No. US20030044851A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029P1
;  CURRENT APPLICATION NUMBER: US/10/012,542
;  CURRENT FILING DATE:  2001-12-12
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
;   LENGTH: 415
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (415)
;   OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring L-amino
;   OTHER INFORMATION: acids
US-10-012-542-134

  Query Match             100.0%;  Score 2130;  DB 4;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-178;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
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Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 9
US-10-115-123-134
; Sequence 134, Application US/10115123
; Publication No. US20030065151A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029G30AP1D2
;  CURRENT APPLICATION NUMBER: US/10/115,123
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: PCT/US99/13418
;  PRIOR FILING DATE: 1999-06-15
;  PRIOR APPLICATION NUMBER: 60/089,507
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,508
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,509
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,510
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/090,112
;  PRIOR FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: 60/090,113
;  PRIOR FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
;  LENGTH: 415
;  TYPE: PRT
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: SITE
;  LOCATION: (415)
;  OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring L-amino acids
US-10-115-123-134

  Query Match           100.0%;  Score 2130;  DB 4;  Length 415;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-178;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 10
US-10-800-834-134
; Sequence 134, Application US/10800834
; Publication No. US20040146930A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029P1D3
;  CURRENT APPLICATION NUMBER: US/10/800,834
;  CURRENT FILING DATE:  2004-03-16
;  PRIOR APPLICATION NUMBER: 10/115,123
;  PRIOR FILING DATE: 2002-04-04
;  PRIOR APPLICATION NUMBER: 09/461,325
;  PRIOR FILING DATE: 1999-12-14
;  PRIOR APPLICATION NUMBER: PCT/US99/13418
;  PRIOR FILING DATE: 1999-06-15
;  PRIOR APPLICATION NUMBER: 60/089,507
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,508
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,509
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,510
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/090,112
;  PRIOR FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: 60/090,113
;  PRIOR FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
;  LENGTH: 415
;  TYPE: PRT
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: SITE
;  LOCATION: (415)
;  OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring L-amino acids
US-10-800-834-134

  Query Match           100.0%;  Score 2130;  DB 4;  Length 415;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-178;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 11
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US-10-276-774-2202
; Sequence 2202, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  APPLICANT:  Tang, Y, Tom et al
;  TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
;  FILE REFERENCE: 21272-030
;  CURRENT APPLICATION NUMBER: US/10/276,774
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 09/560,875
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 09/496,914
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 2700
;  SOFTWARE: Custom
; SEQ ID NO 2202
;   LENGTH: 431
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-276-774-2202

  Query Match             99.2%;  Score 2114;  DB 4;  Length 431;
  Best Local Similarity   99.3%;  Pred. No. 2.9e-177;
  Matches  411;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         18 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 77

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 137

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 197

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 IESKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 257

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 317

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db        318 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVNKAELKM 377

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 431


RESULT 12
US-09-755-665-57
; Sequence 57, Application US/09755665
; Patent No. US20020107186A1
; GENERAL INFORMATION:
;  APPLICANT: Prayaga, Sudhirdas K.
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Taillon, Bruce E.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  MacDougall, John
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-631
;  CURRENT APPLICATION NUMBER: US/09/755,665
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
;   LENGTH: 361
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)..(361)
;   OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
;   OTHER INFORMATION: specification
US-09-755-665-57

  Query Match             84.4%;  Score 1798;  DB 3;  Length 361;
  Best Local Similarity   96.7%;  Pred. No. 1.5e-149;
  Matches  349;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLH 113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLH 60

Qy        114 EGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMA 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMA 120

Qy        174 QKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKN 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKN 180

Qy        234 SSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFS 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFS 240

Qy        294 RWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 RWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 300

Qy        354 HKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIG 413
              |||||||||           ||||||||||||||||||||||||||||||||||||||||
Db        301 HKAELKMDERXXXXXXXXXXXXLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIG 360

Qy        414 K 414
              |
Db        361 K 361


RESULT 13
US-10-629-248-57
; Sequence 57, Application US/10629248
; Publication No. US20040116671A1
; GENERAL INFORMATION:
;  APPLICANT: Prayaga, Sudhirdas K.
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Taillon, Bruce E.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  MacDougall, John
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-631
;  CURRENT APPLICATION NUMBER: US/10/629,248
;  CURRENT FILING DATE:  2003-07-28
;  PRIOR APPLICATION NUMBER: US/09/755,665
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
;   LENGTH: 361
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)..(361)
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;   OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
;   OTHER INFORMATION: specification
US-10-629-248-57

  Query Match             84.4%;  Score 1798;  DB 4;  Length 361;
  Best Local Similarity   96.7%;  Pred. No. 1.5e-149;
  Matches  349;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLH 113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLH 60

Qy        114 EGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMA 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMA 120

Qy        174 QKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKN 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKN 180

Qy        234 SSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFS 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFS 240

Qy        294 RWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 RWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 300

Qy        354 HKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIG 413
              ||||||||||          ||||||||||||||||||||||||||||||||||||||
Db        301 HKAELKMDERXXXXXXXXXXXXLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIG 360

Qy        414 K 414
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Db        361 K 361


RESULT 14
US-10-037-417-66
; Sequence 66, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
;  APPLICANT: Kekuda, Ramesh
;  APPLICANT:  Alsobrook II, John P
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Lepley, Denise M
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Vernet, Corine A.M.
;  APPLICANT:  Li, Li
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Edinger, Shlomit R
;  APPLICANT:  Sciore, Paul
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Rothenberg, Mark
;  APPLICANT:  Stone, David J
;  APPLICANT:  Boldog, Perenc L
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Anderson, David W
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Miller, Charles E
;  APPLICANT:  Eisen, Andrew J
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-235
;  CURRENT APPLICATION NUMBER: US/10/037,417
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: 60/260,018
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: 60/260,360
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/272,411
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: 60/272,817
;  PRIOR FILING DATE: 2001-03-02
;  PRIOR APPLICATION NUMBER: 60/291,186
;  PRIOR FILING DATE: 2001-05-15
;  PRIOR APPLICATION NUMBER: 60/303,231
;  PRIOR FILING DATE: 2001-07-05
;  PRIOR APPLICATION NUMBER: 60/305,060
;  PRIOR FILING DATE: 2001-07-12
;  PRIOR APPLICATION NUMBER: 60/318,405
;  PRIOR FILING DATE: 2001-09-10
;  PRIOR APPLICATION NUMBER: 60/318,700
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
;   LENGTH: 377
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Serpin
;   OTHER INFORMATION: Consensus Sequence
US-10-037-417-66

  Query Match             39.5%;  Score 842;  DB 4;  Length 377;
  Best Local Similarity   43.7%;  Pred. No. 2.6e-65;
  Matches  163;  Conservative   86;  Mismatches  118;  Indels    6;  Gaps    4;

Qy         45 AKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQ--GF 102
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Db          5 ALKLASANADFAFSLYKELVEQNPDKNIFFSPVSISSALAMLSLGAKGNTATQILEVLGF 64

Qy        103 NFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAET 162
              |  :  | ::|:|| ::: || :    |:|: || ||:|: |:   :||||:|  | :|
Db         65 NLTETSEAEIHQGFQHLLQELNRPDTGLQLTTGNALFVDKSLKLLDEFLEDSKRLYQSEV 124

Qy        163 ILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNV 222
              :| : | |:|||||:: :|| ||| :|::::|  ||::| |||:|: :||  ||| :
Db        125 FSVDFSDPEEAKKQINDWVEKKTQGKIKDLLKDLDSDTVLVLVNYIYFKGKWKKPFDPEL 184

Qy        223 TKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITA-IFILPDE-GKL 280
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Db        185 TEEEDFHVDKKTTVKVPMMNQLGTFYYFRDEELNCKVLELPYKGNATSMLFILPDEVGKL 244

Qy        281 KHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTK 340
              : :|  | :|  :|   :  | |:: :|:  : ||:|||  |: :|:: :|    ||:
Db        245 EQVEAALSPETLRKWLENMEPREVELYLPKFSIEGTYDLKDVLAKLGITDLFSNQADLSG 304

Qy        341 IAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPMETP--LVVKIDKPYLLLIYSEK 398
              |:    ||| :||||| |::|| ||| || |||  :|   |  |    |:|:|  ||| :
Db        305 ISEDEDLKVSKAVHKAVLEVDEEGTEAAAATGAIIVPRSLPPELEFTADRPFLFLIYDDP 364

Qy        399 IPSVLFLGKIVNP 411
              |:||:||:|||
Db        365 TGSILFMGKVVNP 377


RESULT 15
US-10-023-634-87
; Sequence 87, Application US/10023634
; Publication No. US20030236389A1
; GENERAL INFORMATION:
;  APPLICANT: Shimkets, Richard A
;  APPLICANT:  Colman, Steven D
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Ballinger, Robert A
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Shenoy, Suresh G
```

```
;  APPLICANT:  Li, Li
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Zerhusen, Bryan D
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Casman, Stacie J
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Gusev, Vladimir Y
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Edinger, Shlomit R
;  APPLICANT:  Gangolli, Esha A
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Gunther, Erik
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Gerlach, Valerie
;  TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
;  TITLE OF INVENTION:  Using the Same
;  FILE REFERENCE: 21402-221
;  CURRENT APPLICATION NUMBER: US/10/023,634
;  CURRENT FILING DATE:  2002-06-28
;  PRIOR APPLICATION NUMBER: 60/256,025
;  PRIOR FILING DATE: 2000-12-15
;  PRIOR APPLICATION NUMBER: 60/265,163
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: 60/272,929
;  PRIOR FILING DATE: 2001-03-02
;  PRIOR APPLICATION NUMBER: 60/274,864
;  PRIOR FILING DATE: 2001-03-09
;  PRIOR APPLICATION NUMBER: 60/276,688
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,880
;  PRIOR FILING DATE: 2001-03-22
;  PRIOR APPLICATION NUMBER: 60/286,409
;  PRIOR FILING DATE: 2001-04-25
;  PRIOR APPLICATION NUMBER: 60/309,246
;  PRIOR FILING DATE: 2001-07-31
;  PRIOR APPLICATION NUMBER: 60/315,600
;  PRIOR FILING DATE: 2001-08-29
;  NUMBER OF SEQ ID NOS: 132
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
;   LENGTH: 371
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-023-634-87

  Query Match             39.4%;  Score 840;  DB 4;  Length 371;
  Best Local Similarity   43.7%;  Pred. No. 3.8e-65;
  Matches  162;  Conservative   86;  Mismatches  117;  Indels    6;  Gaps    4;

Qy         47 ELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQ--GFNF 104
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Db          1 KLASANADFAFSLYKELVEQNPDKNIFFSPVSISSALAMLSLGAKGNTATQILEVLGFNL 60

Qy        105 RKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETIL 164
              :  | ::|:|| ::: || :    |:|: || ||:|: |:   :||||:|  | :|
Db         61 TETSEAEIHQGFQHLLQELNRPDTGLQLTTGNALFVDKSLKLLDEFLEDSKRLYQSEVFS 120

Qy        165 TNFQNLEMAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTK 224
              :| : | |:|||||:: :|| ||| :|::::|  ||::| |||:|: :||  ||| :|:
Db        121 VDFSDPEEAKKQINDWVEKKTQGKIKDLLKDLDSDTVLVLVNYIYFKGKWKKPFDPELTE 180

Qy        225 EEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITA-IFILPDE-GKLKH 282
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Db        181 EEDFHVDKKTTVKVPMMNQLGTFYYFRDEELNCKVLELPYKGNATSMLFILPDEVGKLEQ 240

Qy        283 LEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIA 342
              :|  |  :|  :|   :  | |:: :|:  : ||:|||  |: :|:: :|    ||: |:
Db        241 VEAALSPETLRKWLENMEPREVELYLPKFSIEGTYDLKDVLAKLGITDLFSNQADLSGIS 300

Qy        343 PHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPMETP--LVVKIDKPYLLLIYSEKIP 400
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Db        301 EDEDLKVSKAVHKAVLEVDEEGTEAAAATGAIIVPRSLPPELEFTADRPFLFLIYDDPTG 360

Qy        401 SVLFLGKIVNP 411
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Db        361 SILFMGKVVNP 371


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Job time : 169 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 09:52:00 ; Search time 24 Seconds
(without alignments)
525.123 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 2130
Sequence: 1 MNPTLGLAIFLAVLLTVKGL.....YSEKIPSVLFLGKIVNPIGK 414

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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7: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	842	39.5	377	7	US-11-019-711-66	Sequence 66, Appl
2	786	36.9	418	6	US-10-995-561-753	Sequence 753, App
3	786	36.9	418	6	US-10-995-561-754	Sequence 754, App
4	786	36.9	418	6	US-10-995-561-755	Sequence 755, App
5	786	36.9	418	6	US-10-995-561-756	Sequence 756, App
6	786	36.9	418	6	US-10-995-561-757	Sequence 757, App
7	786	36.9	418	6	US-10-995-561-758	Sequence 758, App
8	786	36.9	418	6	US-10-995-561-759	Sequence 759, App
9	785	36.9	418	7	US-11-177-506-27	Sequence 27, Appl
10	785	36.9	418	7	US-11-183-205-22	Sequence 22, Appl
11	772.5	36.3	360	7	US-11-019-711-67	Sequence 67, Appl
12	765.5	35.9	415	7	US-11-044-224-19	Sequence 19, Appl
13	723.5	34.0	406	6	US-10-995-561-748	Sequence 748, App
14	723.5	34.0	406	6	US-10-995-561-749	Sequence 749, App
15	723.5	34.0	406	6	US-10-995-561-750	Sequence 750, App
16	723.5	34.0	406	6	US-10-995-561-751	Sequence 751, App
17	723.5	34.0	406	6	US-10-995-561-752	Sequence 752, App
18	706	33.1	448	7	US-11-072-512-3380	Sequence 3380, Ap
19	703.5	33.0	417	7	US-11-147-047-39	Sequence 39, Appl
20	703.5	33.0	423	6	US-10-995-561-794	Sequence 794, App
21	703.5	33.0	423	6	US-10-995-561-795	Sequence 795, App
22	703.5	33.0	448	6	US-10-995-561-793	Sequence 793, App
23	690.5	32.4	417	7	US-11-219-282-23	Sequence 23, Appl
24	663.5	31.2	403	7	US-11-219-282-24	Sequence 24, Appl
25	575	27.0	444	6	US-10-131-826A-498	Sequence 498, App
26	575	27.0	444	6	US-10-973-115B-498	Sequence 498, App
27	575	27.0	444	7	US-11-071-580-1	Sequence 1, Appli
28	574	26.9	444	6	US-10-995-561-834	Sequence 834, App
29	574	26.9	444	6	US-10-995-561-835	Sequence 835, App
30	574	26.9	484	6	US-10-995-561-833	Sequence 833, App
31	568	26.7	457	6	US-10-995-561-797	Sequence 797, App
32	479.5	22.5	390	7	US-11-219-282-13	Sequence 13, Appl
33	471.5	22.1	390	7	US-11-019-711-65	Sequence 65, Appl
34	471.5	22.1	390	7	US-11-219-282-12	Sequence 12, Appl
35	467	21.9	366	6	US-10-215-245A-2	Sequence 2, Appli
36	466.5	21.9	376	6	US-10-501-035-283	Sequence 283, App
37	465.5	21.9	374	6	US-10-995-561-668	Sequence 668, App
38	465.5	21.9	374	6	US-10-995-561-669	Sequence 669, App
39	463.5	21.8	376	6	US-10-995-561-844	Sequence 844, App
40	463.5	21.8	376	6	US-10-995-561-848	Sequence 848, App
41	463.5	21.8	380	6	US-10-995-561-846	Sequence 846, App
42	463.5	21.8	390	6	US-10-995-561-847	Sequence 847, App
43	460	21.6	395	6	US-10-453-372-554	Sequence 554, App
44	457	21.5	397	7	US-11-219-282-11	Sequence 11, Appl
45	447	21.0	379	7	US-11-219-282-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-11-019-711-66
; Sequence 66, Application US/11019711
; Publication No. US20060009634A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/11/019,711
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/10/037,417
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231

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;  PRIOR FILING DATE: 2001-07-05
;  PRIOR APPLICATION NUMBER: 60/305,060
;  PRIOR FILING DATE: 2001-07-12
;  PRIOR APPLICATION NUMBER: 60/318,405
;  PRIOR FILING DATE: 2001-09-10
;  PRIOR APPLICATION NUMBER: 60/318,700
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
;   LENGTH: 377
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Serpin
;   OTHER INFORMATION: Consensus Sequence
US-11-019-711-66

  Query Match            39.5%;  Score 842;  DB 7;  Length 377;
  Best Local Similarity  43.7%;  Pred. No. 1e-60;
  Matches  163;  Conservative   86;  Mismatches  118;  Indels    6;  Gaps    4;

Qy         45 AKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQ--GF 102
                | :||  | |  | | |:|   || :||| ||:|||:| :|| |||: :|  :| :  ||
Db          5 ALKLASANADFAFSLYKELVEQNPDKNIFFSPVSISSALAMLSLGAKGNTATQILEVLGF 64

Qy        103 NFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAET 162
              |  :  | ::|:|| ::: || :    |:|: || ||:|: |:   :||||:|  | :|
Db         65 NLTETSEAEIHQGFQHLLQELNRPDTGLQLTTGNALFVDKSLKLLDEFLEDSKRLYQSEV 124

Qy        163 ILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNV 222
                :| : | |:|||||:: :|| ||| :|::::|  ||::| |||:|: :||  ||| :
Db        125 FSVDFSDPEEAKKQINDWVEKKTQGKIKDLLKDLDSDTVLVLVNYIYFKGKWKKPFDPEL 184

Qy        223 TKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITA-IFILPDE-GKL 280
              |:|||| ::| ::|||||| : | :    |::|:| :||:||: | |: :|||||| |||
Db        185 TEEEDFHVDKKTTVKVPMMNQLGTFYYFRDEELNCKVLELPYKGNATSMLFILPDEVGKL 244

Qy        281 KHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTK 340
              : :|  |  :|  :|    :  | |:: :|:  : ||:|||  |: :|:: :|    ||:
Db        245 EQVEAALSPETLRKWLENMEPREVELYLPKFSIEGTYDLKDVLAKLGITDLFSNQADLSG 304

Qy        341 IAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPMETP--LVVKIDKPYLLLIYSEK 398
              |:    ||| :||||| |::|| ||| || |||  :|   |  |    |:|:| ||| :
Db        305 ISEDEDLKVSKAVHKAVLEVDEEGTEAAAATGAIIVPRSLPPELEFTADRPFLFLIYDDP 364

Qy        399 IPSVLFLGKIVNP 411
                |:||:||:|||
Db        365 TGSILFMGKVVNP 377


RESULT 2
US-10-995-561-753
; Sequence 753, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 753
;   LENGTH: 418
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-995-561-753

  Query Match            36.9%;  Score 786;  DB 6;  Length 418;
  Best Local Similarity  42.7%;  Pred. No. 4e-56;
  Matches  155;  Conservative   73;  Mismatches  133;  Indels    2;  Gaps    1;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
                :  | | ::||  :   ||| ||:||:|||:|| || :  | ||| :| ||   ::||
Db         56 EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQ 115

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
              :|||| ::  | |     |:|: || ||: : |:   ||||| |  | :|    || : |
Db        116 IHEGFQELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTE 175

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
              |:|||||:: : | ||| :|:: :|  ||  | |||||: :|:  |:   |:|||| ::
Db        176 EAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVD 235

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
              : ::|||||| | |:: : :  |||  :| : |  | |||| |||||||:|||  | |
Db        236 QATTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 295

Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
               :::     ||   : :|:| :|||:|||  |  :|::|:|    ||: :     ||: :
Db        296 ITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSK 355

Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              ||||| | :||:||| |      : :||  |  || :||:: |:  :   | ||:||:|||
Db        356 AVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNP 415

Qy        412 IGK 414
                |
Db        416 TQK 418


RESULT 3
US-10-995-561-754
; Sequence 754, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 754
;   LENGTH: 418
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-995-561-754

  Query Match            36.9%;  Score 786;  DB 6;  Length 418;
  Best Local Similarity  42.7%;  Pred. No. 4e-56;
  Matches  155;  Conservative   73;  Mismatches  133;  Indels    2;  Gaps    1;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
                :  | | ::||  :   ||| ||:||:|||:|| || :  | ||| :| ||   ::||
Db         56 EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQ 115

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
              :|||| ::  | |     |:|: || ||: : |:   ||||| |  | :|    || : |
Db        116 IHEGFQELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTE 175

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
              |:|||||:: : | ||| :|:: :|  ||  | |||||: :|:  |:   |:|||| ::
Db        176 EAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVD 235

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
              : ::|||||| | |:: : :  |||  :| : |  | |||| |||||||:|||  | |
Db        236 QATTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 295

Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
               :::     ||   : :|:| :|||:|||  |  :|::|:|    ||: :     ||: :
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Db        296 ITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSK 355

Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              ||||| | :||:||| |     : :||  |  || :||:: |:  :   | ||:||:|||
Db        356 AVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNP 415

Qy        412 IGK 414
                |
Db        416 TQK 418


RESULT 4
US-10-995-561-755
; Sequence 755, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 755
;   LENGTH: 418
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-995-561-755

  Query Match             36.9%;  Score 786;  DB 6;  Length 418;
  Best Local Similarity   42.7%;  Pred. No. 4e-56;
  Matches  155;  Conservative   73;  Mismatches  133;  Indels    2;  Gaps    1;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
              :  | | ::||  :   ||| ||:||:|||:|| || :  | ||| :| ||   ::||
Db         56 EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQ 115

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
              :|||| ::  | |    |:|: || ||: : |:   ||||| |  | :|    || : |
Db        116 IHEGFQELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTE 175

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
               |:|||||:: : | ||| :|:: :|  ||  | |||||: :|:  |:   |:|||| ::
Db        176 EAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVD 235

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
              : ::|||||| | |:: : :  |||  :| : |  | |||| |||||||:|||  |  |
Db        236 QATTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 295

Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
               :::     ||   : :|:| :|||:|||  |  :|::|:|    ||: :     ||: :
Db        296 ITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSK 355

Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              ||||| | :||:||| |     : :||  |  || :||:: |:  :   | ||:||:|||
Db        356 AVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNP 415

Qy        412 IGK 414
                |
Db        416 TQK 418


RESULT 5
US-10-995-561-756
; Sequence 756, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 756
;   LENGTH: 418
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-995-561-756

  Query Match             36.9%;  Score 786;  DB 6;  Length 418;
  Best Local Similarity   42.7%;  Pred. No. 4e-56;
  Matches  155;  Conservative   73;  Mismatches  133;  Indels    2;  Gaps    1;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
              :  | | ::||  :   ||| ||:||:|||:|| || :  | ||| :| ||   ::||
Db         56 EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQ 115

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
              :|||| ::  | |    |:|: || ||: : |:   ||||| |  | :|    || : |
Db        116 IHEGFQELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTE 175

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
               |:|||||:: : | ||| :|:: :|  ||  | |||||: :|:  |:   |:|||| ::
Db        176 EAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVD 235

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
              : ::|||||| | |:: : :  |||  :| : |  | |||| |||||||:|||  |  |
Db        236 QATTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 295

Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
               :::     ||   : :|:| :|||:|||  |  :|::|:|    ||: :     ||: :
Db        296 ITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSK 355

Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              ||||| | :||:||| |     : :||  |  || :||:: |:  :   | ||:||:|||
Db        356 AVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNP 415

Qy        412 IGK 414
                |
Db        416 TQK 418


RESULT 6
US-10-995-561-757
; Sequence 757, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 757
;   LENGTH: 418
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-995-561-757

  Query Match             36.9%;  Score 786;  DB 6;  Length 418;
  Best Local Similarity   42.7%;  Pred. No. 4e-56;
  Matches  155;  Conservative   73;  Mismatches  133;  Indels    2;  Gaps    1;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
              :  | | ::||  :   ||| ||:||:|||:|| || :  | ||| :| ||   ::||
Db         56 EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQ 115

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
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Db        116 IHEGFQELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTE 175

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231

Db        176 EAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVD 235

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291

Db        236 QATTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 295

Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351

Db        296 ITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSK 355

Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411

Db        356 AVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNP 415

Qy        412 IGK 414

Db        416 TQK 418


RESULT 7
US-10-995-561-758
; Sequence 758, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 758
;   LENGTH: 418
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-995-561-758

  Query Match           36.9%;  Score 786;  DB 6;  Length 418;
  Best Local Similarity   42.7%;  Pred. No. 4e-56;
  Matches  155;  Conservative   73;  Mismatches  133;  Indels    2;  Gaps    1;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111

Db         56 EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQ 115

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171

Db        116 IHEGFQELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTE 175

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231

Db        176 EAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVD 235

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291

Db        236 QATTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 295

Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351

Db        296 ITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSK 355

Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411

Db        356 AVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNP 415

Qy        412 IGK 414

Db        416 TQK 418


RESULT 8
US-10-995-561-759
; Sequence 759, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 759
;   LENGTH: 418
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-995-561-759

  Query Match           36.9%;  Score 786;  DB 6;  Length 418;
  Best Local Similarity   42.7%;  Pred. No. 4e-56;
  Matches  155;  Conservative   73;  Mismatches  133;  Indels    2;  Gaps    1;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111

Db         56 EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQ 115

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171

Db        116 IHEGFQELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTE 175

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231

Db        176 EAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVD 235

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291

Db        236 QATTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 295

Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351

Db        296 ITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSK 355

Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411

Db        356 AVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNP 415

Qy        412 IGK 414

Db        416 TQK 418


RESULT 9
US-11-177-506-27
; Sequence 27, Application US/11177506
; Publication No. US20060029956A1
; GENERAL INFORMATION:
;  APPLICANT: Beyer, Wayne F.
;  APPLICANT:  Venetta, Thomas M.
;  APPLICANT:  Groelke, John W.
;  APPLICANT:  Blaesius, Rainer H.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
;  TITLE OF INVENTION:  DETECTION OF OVARIAN DISEASE
;  FILE REFERENCE: 46143/294851
;  CURRENT APPLICATION NUMBER: US/11/177,506
;  CURRENT FILING DATE:  2005-07-08
;  PRIOR APPLICATION NUMBER: 60/586,856
;  PRIOR FILING DATE: 2004-07-09
```

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;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
;   LENGTH: 418
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-177-506-27

  Query Match           36.9%;  Score 785;  DB 7;  Length 418;
  Best Local Similarity   42.7%;  Pred. No. 4.9e-56;
  Matches  155;  Conservative   73;  Mismatches  133;  Indels    2;  Gaps    1;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
              :  | | ::||  :   ||| ||:||:|||:|| || :  | ||| :| ||   ::||
Db         56 EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQ 115

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
              :|||| ::  | |    |:|: || ||: : |:   ||||| |  | :|    || : |
Db        116 IHEGFQELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTE 175

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
              |:|||||:: : | ||| :|:: :|  ||  | |||||: :|:  |:   |:|||| ::
Db        176 EAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVD 235

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
              : ::|||||| | |:: : :  |||  :| : |  | |||| |||||||:|||  |  |
Db        236 QVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 295

Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
               :::     ||   : :|:| :|||:|||  |  :|::|:|    ||: :     ||: :
Db        296 ITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSK 355

Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              ||||| | :||:||| |     : :||  |  || :||:: |:  :   | ||:|||:|||
Db        356 AVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNP 415

Qy        412 IGK 414
              |||
Db        416 TQK 418


RESULT 10
US-11-183-205-22
; Sequence 22, Application US/11183205
; Publication No. US20060030521A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Bowe, Caryn
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
;  FILE REFERENCE: 040853-01-5052-US01
;  CURRENT APPLICATION NUMBER: US/11/183,205
;  CURRENT FILING DATE:  2005-07-15
;  PRIOR APPLICATION NUMBER: US 11/183,205
;  PRIOR FILING DATE: 2005-07-15
;  PRIOR APPLICATION NUMBER: US 60/334,233
;  PRIOR FILING DATE: 2001-11-28
;  PRIOR APPLICATION NUMBER: US 60/334,301
;  PRIOR FILING DATE: 2001-11-28
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  PRIOR APPLICATION NUMBER: PCT/US2002/032263
;  PRIOR FILING DATE: 2002-10-09
;  PRIOR APPLICATION NUMBER: US 10/287,994
;  PRIOR FILING DATE: 2002-11-05
;  NUMBER OF SEQ ID NOS: 62
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
;   LENGTH: 418
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-183-205-22

  Query Match           36.9%;  Score 785;  DB 7;  Length 418;
  Best Local Similarity   42.7%;  Pred. No. 4.9e-56;
  Matches  155;  Conservative   73;  Mismatches  133;  Indels    2;  Gaps    1;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
              :  | | ::||  :   ||| ||:||:|||:|| || :  | ||| :| ||   ::||
Db         56 EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQ 115

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
              :|||| ::  | |    |:|: || ||: : |:   ||||| |  | :|    || : |
Db        116 IHEGFQELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTE 175

Qy        172 MAQKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLE 231
              |:|||||:: : | ||| :|:: :|  ||  | |||||: :|:  |:   |:|||| ::
Db        176 EAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVD 235

Qy        232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDT 291
              : ::|||||| | |:: : :  |||  :| : |  | |||| |||||||:|||  |  |
Db        236 QVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI 295

Qy        292 FSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGE 351
               :::     ||   : :|:| :|||:|||  |  :|::|:|    ||: :     ||: :
Db        296 ITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSK 355

Qy        352 AVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              ||||| | :||:||| |     : :||  |  || :||:: |:  :   | ||:|||:|||
Db        356 AVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNP 415

Qy        412 IGK 414
              |||
Db        416 TQK 418


RESULT 11
US-11-019-711-67
; Sequence 67, Application US/11019711
; Publication No. US20060009634A1
; GENERAL INFORMATION:
;  APPLICANT: Kekuda, Ramesh
;  APPLICANT:  Alsobrook II, John P
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Lepley, Denise M
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Vernet, Corine A.M.
;  APPLICANT:  Li, Li
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Edinger, Shlomit R
;  APPLICANT:  Sciore, Paul
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Rothenberg, Mark
;  APPLICANT:  Stone, David J
;  APPLICANT:  Boldog, Ferenc L
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Anderson, David W
;  APPLICANT:  Padigaru, Muralidhara
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;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Miller, Charles E
;  APPLICANT:  Eisen, Andrew J
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-235
;  CURRENT APPLICATION NUMBER: US/11/019,711
;  CURRENT FILING DATE:  2004-12-21
;  PRIOR APPLICATION NUMBER: US/10/037,417
;  PRIOR FILING DATE: 2002-09-20
;  PRIOR APPLICATION NUMBER: 60/260,018
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: 60/260,360
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/272,411
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: 60/272,817
;  PRIOR FILING DATE: 2001-03-02
;  PRIOR APPLICATION NUMBER: 60/291,186
;  PRIOR FILING DATE: 2001-05-15
;  PRIOR APPLICATION NUMBER: 60/303,231
;  PRIOR FILING DATE: 2001-07-05
;  PRIOR APPLICATION NUMBER: 60/305,060
;  PRIOR FILING DATE: 2001-07-12
;  PRIOR APPLICATION NUMBER: 60/318,405
;  PRIOR FILING DATE: 2001-09-10
;  PRIOR APPLICATION NUMBER: 60/318,700
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Serpin
;   OTHER INFORMATION: Consensus Sequence
US-11-019-711-67

  Query Match             36.3%;  Score 772.5;  DB 7;  Length 360;
  Best Local Similarity   41.9%;  Pred. No. 4.1e-55;
  Matches  151;  Conservative   85;  Mismatches  119;  Indels    5;  Gaps    4;

Qy         57 FKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQ--GFNFRKMPEKDLHE 114
              | | |:||  :| :||| ||:|||:| :|| |||: ||  :| :  ||| :  | |:|:
Db          1 FDLYKELAKESPDKNIFFSPVSISSALAMLSLGAKGSTATQILEVLGFNLTETSEADIHQ 60

Qy        115 GFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQN-LEMA 173
              || :::| | :    |:|   | ||:|: |:    |||| |  | ||    :| :  | |
Db         61 GFQHLLHLLNRPDNKLQLKTANALFVDKSLKLLDSFLEDVKKLYGAEVQSVDFSDPAEEA 120

Qy        174 QKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKN 233
              :|||||:: :|| ||| :|: ::|| | ::| | |:|: :||  |||  |:||||::::
Db        121 KKQINDWVKKKTQGKIKDLLSDLDPDTRLVLVNAIYFKGKWKTPFDPENTREEDFYVDET 180

Qy        234 SSVKVPMMFRSG-IYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTF 292
              ::|||||| ::|  :: | |::|:| :||:||: | : : ||||||  |: :|| |  :|
Db        181 TTVKVPMMSQTGRTFRYGRDEELNCQVLELPYKGNASMLIILPDEGGLETVEKALTPETL 240

Qy        293 SRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEA 352
              :|   |::| |:: :|:  :  ::|||  |  :|:: :|    ||: |:  : ||| :
Db        241 KKWTKSLTKRSVELYLPKFKLEISYDLKDVLEKLGITDLFSNKADLSGISEDKDLKVSKV 300

Qy        353 VHKAELKMDERGTEGAAGTGAQTLPME-TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              |||| |:::| ||| || ||   :|    |   | ::|:| ||       |:||:||:|||
Db        301 VHKAFLEVNEEGTEAAAATGVIIVPRSLPPPEFKANRPFLFLIRDNPTGSILFMGKVVNP 360


RESULT 12
US-11-044-224-19
; Sequence 19, Application US/11044224
; Publication No. US20060040867A1
; GENERAL INFORMATION:
;  APPLICANT: Shapiro, Leland
;  TITLE OF INVENTION: Inhibitors of Serine Protease Activity and Their Use in Methods
;  TITLE OF INVENTION:  and Compositions for Treatment of Bacterial Infections
;  FILE REFERENCE: 114232.107
;  CURRENT APPLICATION NUMBER: US/11/044,224
;  CURRENT FILING DATE:  2005-01-28
;  PRIOR APPLICATION NUMBER: 60/123,167
;  PRIOR FILING DATE: 1999-03-05
;  PRIOR APPLICATION NUMBER: 60/137,795
;  PRIOR FILING DATE: 1999-06-03
;  PRIOR APPLICATION NUMBER: 09/518,098
;  PRIOR FILING DATE: 2000-03-03
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
;   LENGTH: 415
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-044-224-19

  Query Match             35.9%;  Score 765.5;  DB 7;  Length 415;
  Best Local Similarity   42.6%;  Pred. No. 1.8e-54;
  Matches  155;  Conservative   72;  Mismatches  130;  Indels    7;  Gaps    3;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFR--KMPEKD 111
              :  | | ::||       ||| ||:||:|||:|| || :  | ||| :| ||   ::||
Db         56 EFAFSLYRQLA----STNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQ 111

Qy        112 LHEGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLE 171
              :|||  ::  | |     |:|: || ||: : |:   ||||| |  | :|    || : |
Db        112 IHEGFQELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTE 171

Qy        172 MAQKQ-INDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFL 230
               |:|| |||:: : | ||| :|:: :|  ||  | |||||: :|:  |:   |:|||| :
Db        172 EAKKQTINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHV 231

Qy        231 EKNSSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVD 290
              :: ::|||||| | |:: : :  |||  :| : |  | |||| |||||||:|||  |  |
Db        232 DQVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHD 291

Qy        291 TFSRWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVG 350
              :::     ||   : :|:| :|||:|||  |  :|::|:|    ||: :     ||:
Db        292 IITKPLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLS 351

Qy        351 EAVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVN 410
              :||||| | :||:||| |      : :||  |  || :||:: |:  :   | ||:||:||
Db        352 KAVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVN 411

Qy        411 PIGK 414
              |  |
Db        412 PTQK 415


RESULT 13
US-10-995-561-748
; Sequence 748, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 748
;   LENGTH: 406
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-995-561-748

  Query Match             34.0%;  Score 723.5;  DB 6;  Length 406;
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Best Local Similarity 37.0%; Pred. No. 4.6e-51;
Matches 153; Conservative 88; Mismatches 156; Indels 17; Gaps 6;

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Qy          7 LAIFL---AVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKL 63
              : :||    |||: :|       ||  |   |       : |         | | | : |
Db          1 MQLFLLLCLVLLSPQGASLHRHHPREMKKRVE----DLHVGATVAPSSRRDFTFDLYRAL 56

Qy         64 AFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQ--GFNFRKMPEKDLHEGFHYIIH 121
              |   | ::|| ||:||| : :|| |||  ||  :| :  | | :|  ||:|| ||  ::
Db         57 ASAAPSQSIFFSPVSISMSLAMLSLGAGSSTKMQILEGLGLNLQKSSEKELHRGFQQLLQ 116

Qy        122 ELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFI 181
              || |     :||:|| || |  :  |  |:   |  | |:|  |||::   | |||||::
Db        117 ELNQPRDGFQLSLGNALFTDLVVDLQDTFVSAMKTLYLADTFPTNFRDSAGAMKQINDYV 176

Qy        182 SQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMM 241
              :::| ||| :|::|:|   |::: |||||:|:|:  |:   |:|:||::   : |:||||
Db        177 AKQTKGKIVDLLKNLDSNAVVIMVNYIFFKAKWETSFNHKGTQEQDFYVTSETVVRVPMM 236

Qy        242 FRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSR 301
              |   |    | ||| :: :||| | ||:|||| |||:: :| ||   | :|  :  :
Db        237 SREDQYHYLLDRNLSCRVVGVPYQGNATALFILPSEGKMQQVENGLSEKTLRKWLKMFKK 296

Qy        302 RVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMD 361
              | ::: :|:  : |:: |:| |  :|:| :|  | ||: |: | :::| | |||| :::|
Db        297 RQLELYLPKFSIEGSYQLEKVLPSLGISNVFTSHADLSGISNHSNIQVSEMVHKAVVEVD 356

Qy        362 ERGTEGAAGTGA----QTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              | ||  || ||      ::  : :  :|  ::|:|: |       ::|||||:  |
Db        357 ESGTRAAAATGTIFTFRSARLNSQRLV-FNRPFLMFIVDN---NILFLGKVNRP 406
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RESULT 14
US-10-995-561-749
; Sequence 749, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 749
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-749

Query Match 34.0%; Score 723.5; DB 6; Length 406;
Best Local Similarity 37.0%; Pred. No. 4.6e-51;
Matches 153; Conservative 88; Mismatches 156; Indels 17; Gaps 6;

```
Qy          7 LAIFL---AVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKL 63
              : :||    |||: :|       ||  |   |       : |         | | | : |
Db          1 MQLFLLLCLVLLSPQGASLHRHHPREMKKRVE----DLHVGATVAPSSRRDFTFDLYRAL 56

Qy         64 AFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQ--GFNFRKMPEKDLHEGFHYIIH 121
              |   | ::|| ||:||| : :|| |||  ||  :| :  | | :|  ||:|| ||  ::
Db         57 ASAAPSQSIFFSPVSISMSLAMLSLGAGSSTKMQILEGLGLNLQKSSEKELHRGFQQLLQ 116

Qy        122 ELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFI 181
              || |     :||:|| || |  :  |  |:   |  | |:|  |||::   | |||||::
Db        117 ELNQPRDGFQLSLGNALFTDLVVDLQDTFVSAMKTLYLADTFPTNFRDSAGAMKQINDYV 176

Qy        182 SQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMM 241
              :::| ||| :|::|:|   |::: |||||:|:|:  |:   |:|:||::   : |:||||
Db        177 AKQTKGKIVDLLKNLDSNAVVIMVNYIFFKAKWETSFNHKGTQEQDFYVTSETVVRVPMM 236

Qy        242 FRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSR 301
              |   |    | ||| :: :||| | ||:|||| |||:: :| ||   | :|  :  :
Db        237 SREDQYHYLLDRNLSCRVVGVPYQGNATALFILPSEGKMQQVENGLSEKTLRKWLKMFKK 296

Qy        302 RVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMD 361
              | ::: :|:  : |:: |:| |  :|:| :|  | ||: |: | :::| | |||| :::|
Db        297 RQLELYLPKFSIEGSYQLEKVLPSLGISNVFTSHADLSGISNHSNIQVSEMVHKAVVEVD 356

Qy        362 ERGTEGAAGTGA----QTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              | ||  || ||      ::  : :  :|  ::|:|: |       ::|||||:  |
Db        357 ESGTRAAAATGTIFTFRSARLNSQRLV-FNRPFLMFIVDN---NILFLGKVNRP 406
```

RESULT 15
US-10-995-561-750
; Sequence 750, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 750
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-750

Query Match 34.0%; Score 723.5; DB 6; Length 406;
Best Local Similarity 37.0%; Pred. No. 4.6e-51;
Matches 153; Conservative 88; Mismatches 156; Indels 17; Gaps 6;

```
Qy          7 LAIFL---AVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKL 63
              : :||    |||: :|       ||  |   |       : |         | | | : |
Db          1 MQLFLLLCLVLLSPQGASLHRHHPREMKKRVE----DLHVGATVAPSSRRDFTFDLYRAL 56

Qy         64 AFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQ--GFNFRKMPEKDLHEGFHYIIH 121
              |   | ::|| ||:||| : :|| |||  ||  :| :  | | :|  ||:|| ||  ::
Db         57 ASAAPSQSIFFSPVSISMSLAMLSLGAGSSTKMQILEGLGLNLQKSSEKELHRGFQQLLQ 116

Qy        122 ELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFI 181
              || |     :||:|| || |  :  |  |:   |  | |:|  |||::   | |||||::
Db        117 ELNQPRDGFQLSLGNALFTDLVVDLQDTFVSAMKTLYLADTFPTNFRDSAGAMKQINDYV 176

Qy        182 SQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMM 241
              :::| ||| :|::|:|   |::: |||||:|:|:  |:   |:|:||::   : |:||||
Db        177 AKQTKGKIVDLLKNLDSNAVVIMVNYIFFKAKWETSFNHKGTQEQDFYVTSETVVRVPMM 236

Qy        242 FRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSR 301
              |   |    | ||| :: :||| | ||:|||| |||:: :| ||   | :|  :  :
Db        237 SREDQYHYLLDRNLSCRVVGVPYQGNATALFILPSEGKMQQVENGLSEKTLRKWLKMFKK 296

Qy        302 RVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMD 361
              | ::: :|:  : |:: |:| |  :|:| :|  | ||: |: | :::| | |||| :::|
Db        297 RQLELYLPKFSIEGSYQLEKVLPSLGISNVFTSHADLSGISNHSNIQVSEMVHKAVVEVD 356

Qy        362 ERGTEGAAGTGA----QTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNP 411
              | ||  || ||      ::  : :  :|  ::|:|: |       ::|||||:  |
Db        357 ESGTRAAAATGTIFTFRSARLNSQRLV-FNRPFLMFIVDN---NILFLGKVNRP 406
```

Search completed: March 31, 2006, 09:55:06
Job time : 25 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 09:54:55 ; Search time 221.073 Seconds
(without alignments)
822.818 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 414
Sequence: 1 MNPTLGLAIFLAVLLTVKGL.....YSEKIPSVLFLGKIVNPIGK 414

Scoring table: OLIGOM
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 15

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	414	100.0	414	4	AAU05754	Aau05754 Human NOV
2	414	100.0	414	4	AAE04885	Aae04885 Human pro
3	414	100.0	414	6	ADA57300	Ada57300 Human sec
4	414	100.0	414	6	ADA41179	Ada41179 Human sec
5	414	100.0	414	8	ADN05952	Adn05952 Antipsori
6	414	100.0	415	3	AAY86217	Aay86217 Human sec
7	414	100.0	415	6	ABO53360	Abo53360 Novel hum
8	353	85.3	414	4	AAM78898	Aam78898 Human pro
9	310	74.9	358	4	AAU05759	Aau05759 Human NOV
10	181	43.7	431	4	ABB11832	Abb11832 Human sec
11	181	43.7	431	4	AAM79882	Aam79882 Human pro
12	129	31.2	140	4	AAM70426	Aam70426 Human bon

ALIGNMENTS

RESULT 1
AAU05754
ID AAU05754 standard; protein; 414 AA.
XX
AC AAU05754;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human NOV7 polypeptide.
XX
KW Human; NOV7; AL132990 B; fertility disorder; spermatogenesis; cardiant;
KW cytostatic; immunomodulatory; antiproliferative; antidiabetic;
KW cell proliferation; cancer; diabetic retinopathy; angiogenic disorder;
KW pulmonary disorder; haematopoietic disorder; immunological disorder;
KW inflammatory disorder; tumour related disorders; emphysema; cirrhosis;
KW wound healing; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200149729-A2.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000299.
XX
PR 06-JAN-2000; 2000US-0174724P.
PR 11-JAN-2000; 2000US-0175434P.
PR 11-JAN-2000; 2000US-0175488P.
PR 12-JAN-2000; 2000US-0175696P.
PR 12-JAN-2000; 2000US-0175743P.
PR 13-JAN-2000; 2000US-0175819P.
PR 07-AUG-2000; 2000US-0223524P.
PR 04-JAN-2001; 2001US-00755665.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Prayaga SK, Majumder K, Taillon BE, Spaderna SK, Spytek KA;
PI Macdougall J;
XX
DR WPI; 2001-418356/44.
DR N-PSDB; AAS10874.
XX
PT Nucleic acids encoding polypeptides, designated NOVX polypeptides, useful
PT for treating a syndrome associated with a NOVX-associated disorder, e.g.
PT cell proliferation (e.g. cancer and diabetic retinopathy), angiogenic or
PT pulmonary disorder.
XX
PS Claim 1; Page 32; 144pp; English.
XX
CC The invention relates to nucleic acids encoding NOVX (X being an integer
CC from 1-8) polypeptides. The NOVX nucleic acids and polypeptides are
CC useful in diagnosing, treating or manufacturing a medicament for a
CC disease or disorder associated with NOVX e.g. cell proliferation (cancer
CC and diabetic retinopathy), angiogenic or pulmonary disorders, fertility
CC disorders (e.g of spermatogenesis), haematopoietic, immunological,
CC inflammatory and tumour related disorders, emphysema, cirrhosis, wound
CC healing. NOVX nucleic acids are also useful in gene therapy. They are
CC also used for screening for a modulator of activity or of latency or
CC predisposition to a NOVX-associated disorder. They are also useful for
CC determining the presence of or predisposition to a NOVX-associated
CC disorder. The present sequence represents NOV7 (AL132990 B), which has
CC sequence homology to an unidentified human secreted protein (HWHGUS54)
CC and to alpha1 anti-trypsin
XX
SQ Sequence 414 AA;

Query Match 100.0%; Score 414; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
```

RESULT 2
AAE04885
ID AAE04885 standard; protein; 414 AA.
XX
AC AAE04885;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human protease protein-12 (PRTS-12).
XX
KW Human; protease protein-12; PRTS-12; cytostatic; hypotensive; antiviral;
KW gastrointestinal disorder; anorexia; dysphagia; cardiovascular disorder;
KW atherosclerosis; vasculitis; autoimmune disorder; inflammatory disorder;
KW Alzheimer's disease; cell proliferative disorder; dermatitis; cirrhosis;
KW acquired immune deficiency syndrome; AIDS; neurological disorder; asthma;
KW developmental disorder; epithelial disorder; eczema; dementia; nootropic;
KW neurological disorder; reproductive disorder; infertility; teratogenesis;
KW immunosuppressive; drug screening; actinic keratosis; cardiant; epilepsy;
KW anaemia; antitumour; gene therapy; antibacterial.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .19
FT /label= Signal_peptide
FT Protein 20. .414
FT /note= "Mature human PRTS-12"
XX
PN WO200146443-A2.
XX
PD 28-JUN-2001.
XX
PF 19-DEC-2000; 2000WO-US034811.
XX
PR 23-DEC-1999; 99US-0172055P.
PR 21-JAN-2000; 2000US-0177334P.
PR 28-JAN-2000; 2000US-0178884P.
PR 02-FEB-2000; 2000US-0179903P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Yang J, Baughn MR, Burford N, Au-Young J, Lu DAM, Reddy R;
PI Yue H, Nguyen DB, Tang YT, Yao MG, Lal P;
XX
DR WPI; 2001-418080/44.
DR N-PSDB; AAD09549.
XX
PT Novel human protease proteins (PRTS) useful for diagnosing, treating,
PT preventing gastrointestinal, cardiovascular, autoimmune/inflammatory,
PT cell proliferative disorders associated with abnormal expression of PRTS.
XX
PS Claim 1; Page 118; 129pp; English.
XX
CC The present sequence is human protease protein (PRTS-12). Human PRTS and
CC its nucleic acid molecule are useful for the diagnosis, treatment and
CC prevention of disorders associated with increased or decreased expression
CC of PRTS. Examples of such disorders include, gastrointestinal disorder
CC such as anorexia, dysphagia; cardiovascular disorder such as
CC atherosclerosis, vasculitis; autoimmune/inflammatory disorder such as
CC acquired immune deficiency syndrome (AIDS), asthma; cell proliferative
CC disorder such as actinic keratosis, cirrhosis; developmental disorder
CC such as epilepsy, anaemia; epithelial disorder such as allergic contact
CC dermatitis, eczema; neurological disorder such as Alzheimer's disease,
CC dementia and reproductive disorder such as infertility and teratogenesis.
CC PRTS DNA is useful for creating 'knockin' humanised animals (pigs) or
CC transgenic animals (mice or rats) to model human disease. PRTS DNA is
CC also in useful is gene therapy. PRTS and its immunogenic fragments are
CC useful for screening libraries of compounds in several drug screening
CC assays. PRTS is useful for analysing the proteome of a tissue or cell
CC type
XX
SQ Sequence 414 AA;

Query Match 100.0%; Score 414; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
```

RESULT 3
ADA57300
ID ADA57300 standard; protein; 414 AA.
XX
AC ADA57300;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted protein #583.
XX
KW immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW cytostatic; cerebroprotective; neuroprotective; nootropic;
KW cardiovascular; antiarteriosclerotic; gene therapy;
KW human secreted protein; immune disorder; inflammation;
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW triple helix formation; antisense gene therapy; forensic biology.
XX
OS Homo sapiens.

XX
PN WO2002102994-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008278.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-167512/16.
DR N-PSDB; ADA56404.
XX
PT New human secreted polypeptides and polynucleotides, useful for
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT conditions, respiratory disorders, cancers, CNS disorders, or
PT neurodegenerative disorders.
XX
PS Claim 13; SEQ ID NO 1490; 1754pp; English.
XX
CC The invention relates to 592 new human secreted polypeptides useful for
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC conditions, respiratory disorders, cancers, CNS disorders, or
CC neurodegenerative disorders, or polypeptides comprising an amino acid
CC sequence at least 95% identical to the new sequences. The polypeptides,
CC antibodies or antibody fragments that bind to the polypeptides, nucleic
CC acids encoding the polypeptides, agonists or antagonists that binds to
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC compositions for diagnosing, treating or preventing an e.g. immune
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC polynucleotides are useful for chromosome identification, chromosome
CC mapping, for controlling gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy, for identifying individuals
CC from minute biological samples, in forensic biology, and as hybridization
CC probes. The polypeptides are useful for as molecular weight markers on
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC gels, to raise antibodies, for testing biological activities, and for
CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to one of the polypeptide of the invention. Note: The sequence data for
CC this patent did form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 414 AA;

Query Match 100.0%; Score 414; DB 6; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
```

RESULT 4
ADA41179
ID ADA41179 standard; protein; 414 AA.
XX
AC ADA41179;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted protein.
XX
KW Human; secreted protein; cancer; hyperproliferative disorder;
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW vulnerary; cardiant; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2002102993-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008123.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-175238/17.
XX
PT New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing,
PT preventing or treating cancer or other hyperproliferative disorder,
PT asthma, allergies or AIDS.
XX
PS Claim 1; SEQ ID NO 1561; 3205pp; English.
XX
CC The invention relates to novel genes ADA39629-ADA40565 and proteins
CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
CC treating or ameliorating medical conditions e.g. by protein or gene
CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
CC fragments, and agonists or antagonists that bind to the polypeptide are
CC useful for preparing a diagnostic or pharmaceutical composition for
CC diagnosing or treating cancer or other hyperproliferative disorder. The
CC polypeptides and nucleic acid molecules are also useful for detecting,
CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
CC or other hyperproliferative disorders including neoplasms, autoimmune
CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
CC thrombocytopenia), allergic reactions including asthma or eczema,

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CC   inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC   bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC   Alzheimer's disease or Parkinson's disease), cardiovascular disorders
CC   (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
CC   fungal or viral infections including HIV/AIDS), or wound healing and
CC   disorders of epithelial cell proliferation. The nucleic acids are also
CC   useful for chromosome identification, radiation hybrid mapping or long-
CC   range restriction mapping, as molecular weight markers, or as
CC   hybridization or diagnostic probes. The polypeptides and antibodies are
CC   useful for providing immunological probes for differential identification
CC   of the tissues immunohistochemistry assays. Note: The sequence data for
CC   this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 414 AA;

  Query Match           100.0%;  Score 414;  DB 6;  Length 414;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 5
ADN05952
ID   ADN05952 standard; protein; 414 AA.
XX
AC   ADN05952;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Antipsoriatic protein sequence #1136.
XX
KW   antipsoriatic; gene therapy; psoriasis; diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO2004028479-A2.
XX
PD   08-APR-2004.
XX
PF   25-SEP-2003; 2003WO-US030907.
XX
PR   25-SEP-2002; 2002US-0414006P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Bodary S,  Clark H,  Jackman J,  Schoenfeld J,  Williams PM,  Wood WI;
PI   Wu TD;
XX
DR   WPI; 2004-305105/28.
DR   N-PSDB; ADN05951.
XX
PT   New PRO nucleic acid or polypeptide, useful for preparing a
PT   pharmaceutical composition for diagnosing or treating psoriasis in a
PT   mammal.
XX
PS   Claim 9; SEQ ID NO 2347; 3069pp; English.
XX
CC   The invention relates to novel polynucleotide and polypeptides for
CC   treating psoriasis or a sequence having at least 80% identity to the
CC   above sequences. The nucleic acid is useful for preparing a composition
CC   for diagnosing or treating psoriasis in a mammal. This sequence
CC   corresponds to one of the polypeptides of the invention.
XX
SQ   Sequence 414 AA;

  Query Match           100.0%;  Score 414;  DB 8;  Length 414;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 6
AAY86217
ID   AAY86217 standard; protein; 415 AA.
XX
AC   AAY86217;
XX
DT   19-APR-2000  (first entry)
XX
DE   Human secreted protein HWHGU54, SEQ ID NO:132.
XX
KW   Human; secreted protein; cancer; tumour; developmental abnormality;
KW   foetal deficiency; blood disorder; immune system disorder; inflammation;
KW   autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW   schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW   atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW   digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
KW   therapy.
XX
OS   Homo sapiens.
```

XX
PN WO9966041-A1.
XX
PD 23-DEC-1999.
XX
PF 15-JUN-1999; 99WO-US013418.
XX
PR 16-JUN-1998; 98US-0089507P.
PR 16-JUN-1998; 98US-0089508P.
PR 16-JUN-1998; 98US-0089509P.
PR 16-JUN-1998; 98US-0089510P.
PR 22-JUN-1998; 98US-0090112P.
PR 22-JUN-1998; 98US-0090113P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Ni J, Rosen CA, Wei Y, Young PE, Florence KA;
PI Soppet DR, Brewer LA, Endress GA, Carter KC, Mucenski M, Ebner R;
PI Lafleur DW, Olsen HS, Shi Y, Moore PA, Komatsoulis G;
XX
DR WPI; 2000-106100/09.
DR N-PSDB; AAZ97021.
XX
PT New isolated human genes and the secreted polypeptides they encode,
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
PS Claim 1; Page 389-390; 586pp; English.
XX
CC AAZ97019 to AAZ97137 represent 94 isolated human secreted protein genes.
CC AAY86215 to AAY86333 are the secreted proteins encoded by the 94 human
CC genes. This sequence represents a fragment of one of the human secreted
CC proteins. The genes and their corresponding secreted polypeptides are
CC useful for preventing, treating or ameliorating medical conditions, e.g.,
CC by protein or gene therapy. Also pathological conditions can be diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new genes. Specific uses are
CC described for each of the 94 genes, based on which tissues they are most
CC highly expressed in, and include developing products for the diagnosis or
CC treatment of cancer, tumours, developmental abnormalities and foetal
CC deficiencies, blood disorders, diseases of the immune system, autoimmune
CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
CC digestive/endocrine disorders, infections and AIDS. The polypeptides are
CC also useful for identifying their binding partners. The sequences shown
CC in AAY86334 to AAY86585 represent fragments of the secreted proteins
XX
SQ Sequence 415 AA;

Query Match 100.0%; Score 414; DB 3; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIPFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIPFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
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RESULT 7
ABO53360
ID ABO53360 standard; protein; 415 AA.
XX
AC ABO53360;
XX
DT 06-NOV-2003 (first entry)
XX
DE Novel human secreted protein #3.
XX
KW Human; vaccine; immune system disorder; haematopoietic cell disorder;
KW cancer; autoimmune disorder; rheumatoid arthritis; glomerulonephritis;
KW HIV infection; anaemia; thrombocytopenia blood coagulation disorder;
KW blood platelet disorder; wound; heart attack; myocardial infarction;
KW stroke; scarring; asthma; graft-versus host rejection; inflammation;
KW hyperproliferative disorder; lymphoproliferative disorder; arrhythmia;
KW aberrant cellular division; cell proliferative disorder; angiogenesis;
KW cardiovascular disorder; pulmonary heart disease; neovascularisation;
KW hypertrophic scar; keloid; ocular disorder; diabetic retinopathy;
KW uveitis; epithelial cell proliferation; neurological disease; apoptosis;
KW Parkinson's disease; Alzheimer's disease; Huntington's chorea; ALS; AIDS;
KW amyotrophic lateral sclerosis; toxin induced liver disease; septic shock;
KW cachexia; anorexia; lung damage; infection.
XX
OS Homo sapiens.
XX
PN US2003065151-A1.
XX
PD 03-APR-2003.
XX
PF 04-APR-2002; 2002US-00115123.
XX
PR 16-JUN-1998; 98US-0089507P.
PR 16-JUN-1998; 98US-0089508P.
PR 16-JUN-1998; 98US-0089509P.
PR 16-JUN-1998; 98US-0089510P.
PR 22-JUN-1998; 98US-0090112P.
PR 22-JUN-1998; 98US-0090113P.
PR 15-JUN-1999; 99WO-US013418.
PR 14-DEC-1999; 99US-00461325.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Ni J, Rosen CA, Wei Y, Young P, Florence K, Soppet DR;
PI Brewer LA, Endress GA, Carter KC, Mucenski M, Ebner R, Lafleur DW;
PI Olsen H, Shi Y, Moore PA, Komatsoulis G;
XX
DR WPI; 2003-531736/50.
DR N-PSDB; ACH66650.
XX
PT Novel antibody that binds specifically to a HCEJQ69 protein, useful for
PT detecting the presence of a protein in a biological sample, and for
PT treating cancers, autoimmune disorders and HIV infection.
XX
PS Disclosure; SEQ ID NO 134; 176pp; English.
XX
CC The invention relates to an isolated antibody or its fragment that
CC specifically binds to a protein. The antibody is useful for detecting a
CC protein in a biological sample, by contacting the biological sample with
CC the antibody or its fragment and detecting the protein in the biological
CC sample. The antibody is useful for purifying, detecting and targeting the
CC human secreted proteins, including both in vitro and in vivo diagnostic
CC and therapeutic methods. The antibody is useful for immunophenotyping of

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CC   cell lines in biological samples and in antibody-based therapies for
CC   treating, inhibiting and preventing diseases, disorders or conditions
CC   associated with aberrant expression and/or activity of the above
CC   proteins. The antibody is useful for treating deficiencies or disorders
CC   of immune system and haematopoietic cells, for increasing differentiation
CC   and proliferation of haematopoietic cells, for treating immune
CC   deficiencies or disorders e.g. cancers, autoimmune disorders (such as
CC   rheumatoid arthritis and glomerulonephritis), HIV infection, anaemia and
CC   thrombocytopenia and as a marker for a particular immune system disease
CC   or disorder. The antibody is also useful for treating blood coagulation
CC   disorders, blood platelet disorders, wounds, heart attacks (infarction),
CC   strokes, scarring and asthma. The antibody is also useful for treating or
CC   preventing graft-versus host rejection, for modulating inflammation, for
CC   treating hyperproliferative disorders e.g. lymphoproliferative disorders
CC   and cancers, for inhibiting aberrant cellular division and for treating
CC   cell proliferative disorders. The antibody is also useful for treating
CC   cardiovascular disorders e.g. pulmonary heart disease and arrhythmia,
CC   disorders associated with neovascularisation and angiogenesis, for
CC   treating hypertrophic scars and keloids, ocular disorders e.g. diabetic
CC   retinopathy and uveitis, for wound healing and disorders of epithelial
CC   cell proliferation. The antibody is also useful for treating neurological
CC   diseases e.g. Parkinson's disease, Alzheimer's disease, Huntington's
CC   chorea and amyotrophic lateral sclerosis (ALS), diseases associated with
CC   increased apoptosis e.g. AIDS, toxin induced liver disease, septic shock,
CC   cachexia and anorexia, for preventing and healing damage to lungs and for
CC   treating infectious diseases. The present sequence represents the amino
CC   acid sequence of a novel human secreted protein. Note: the sequence data
CC   for this patent did not form part of the printed specification but was
CC   obtained in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20030065151
XX
SQ   Sequence 415 AA;

  Query Match             100.0%;  Score 414;  DB 6;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 8
AAM78898
ID   AAM78898 standard; protein; 414 AA.
XX
AC   AAM78898;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human protein SEQ ID NO 1560.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US004098.
XX
PR   03-FEB-2000; 2000US-00496914.
PR   27-APR-2000; 2000US-00560875.
PR   20-JUN-2000; 2000US-00598075.
PR   19-JUL-2000; 2000US-00620325.
PR   01-SEP-2000; 2000US-00654936.
PR   15-SEP-2000; 2000US-00663561.
PR   20-OCT-2000; 2000US-00693325.
PR   30-NOV-2000; 2000US-00728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y;
PI   Ma Y,  Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   N-PSDB; AAK52031.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT   in diagnosis and gene therapy.
XX
PS   Claim 20; Page 3878-3879; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC   (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC   sequence listing were missing at the time of publication
XX
SQ   Sequence 414 AA;

  Query Match             85.3%;  Score 353;  DB 4;  Length 414;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  353;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 353
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 353
```

RESULT 9
AAU05759
ID AAU05759 standard; protein; 358 AA.
XX
AC AAU05759;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human NOV7 polypeptide #2.
XX
KW Human; NOV7; AL132990 B; fertility disorder; spermatogenesis; cardiant;
KW cytostatic; immunomodulatory; antiproliferative; antidiabetic;
KW cell proliferation; cancer; diabetic retinopathy; angiogenic disorder;
KW pulmonary disorder; haematopoietic disorder; immunological disorder;
KW inflammatory disorder; tumour related disorders; emphysema; cirrhosis;
KW wound healing; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 311. .322
FT /label= OTHER
FT /note= "Other= Unknown"
XX
PN WO200149729-A2.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000299.
XX
PR 06-JAN-2000; 2000US-0174724P.
PR 11-JAN-2000; 2000US-0175434P.
PR 11-JAN-2000; 2000US-0175488P.
PR 12-JAN-2000; 2000US-0175696P.
PR 12-JAN-2000; 2000US-0175743P.
PR 13-JAN-2000; 2000US-0175819P.
PR 07-AUG-2000; 2000US-0223524P.
PR 04-JAN-2001; 2001US-00755665.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Prayaga SK, Majumder K, Taillon BE, Spaderna SK, Spytek KA;
PI Macdougall J;
XX
DR WPI; 2001-418356/44.
XX
PT Nucleic acids encoding polypeptides, designated NOVX polypeptides, useful
PT for treating a syndrome associated with a NOVX-associated disorder, e.g.
PT cell proliferation (e.g. cancer and diabetic retinopathy), angiogenic or
PT pulmonary disorder.
XX
PS Disclosure; Page 33; 144pp; English.
XX
CC The invention relates to nucleic acids encoding NOVX (X being an integer
CC from 1-8) polypeptides. The NOVX nucleic acids and polypeptides are
CC useful in diagnosing, treating or manufacturing a medicament for a
CC disease or disorder associated with NOVX e.g. cell proliferation (cancer
CC and diabetic retinopathy), angiogenic or pulmonary disorders, fertility
CC disorders (e.g of spermatogenesis), haematopoietic, immunological,
CC inflammatory and tumour related disorders, emphysema, cirrhosis, wound
CC healing. NOVX nucleic acids are also useful in gene therapy. They are
CC also used for screening for a modulator of activity or of latency or
CC predisposition to a NOVX-associated disorder. They are also useful for
CC determining the presence of or predisposition to a NOVX-associated
CC disorder. The present sequence represents a version of NOV7 (AL132990 B)
CC appearing in table 25 of the specification, which has sequence homology
CC to an unidentified human secreted protein (HWHGUS54) and to alpha1 anti-
CC trypsin
XX
SQ Sequence 358 AA;

```
  Query Match             74.9%;  Score 310;  DB 4;  Length 358;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-294;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLH 113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLH 60

Qy        114 EGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMA 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMA 120

Qy        174 QKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKN 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKN 180

Qy        234 SSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFS 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFS 240

Qy        294 RWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 RWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 300

Qy        354 HKAELKMDER 363
              ||||||||||
Db        301 HKAELKMDER 310
```

RESULT 10
ABB11832
ID ABB11832 standard; peptide; 431 AA.
XX
AC ABB11832;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human secreted protein homologue, SEQ ID NO:2202.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnerary; antiulcer.
XX
OS Homo sapiens.
XX
PN WO200157188-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US003800.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
XX

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PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-457740/49.
DR   N-PSDB; ABA09076.
XX
PT   Human proteins and DNA encoding sequences useful for preventing, treating
PT   or ameliorating a medical condition in a mammalian subject e.g. arthritis
PT   and cancer.
XX
PS   Claim 20; Page 263; 1963pp; English.
XX
CC   Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC   sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC   invention also relates to vectors and recombinant host cells comprising a
CC   nucleotide of the invention, methods of producing the novel polypeptides,
CC   antibodies against the polypeptides, methods of detecting the nucleotides
CC   or polypeptides in a sample, and methods of identifying compounds which
CC   bind to polypeptides of the invention. Although novel, many of the
CC   polypeptides of the invention have homology to known proteins, thereby
CC   giving an insight into their probable biological activities, and hence
CC   potential therapeutic applications. The polypeptides of the invention may
CC   have various activities, including cytokine, cell proliferation or cell
CC   differentiation activities; stem cell growth factor activity;
CC   haematopoiesis regulatory activity; tissue growth activity;
CC   immunomodulatory activity; activin- or inhibin-related activities;
CC   chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC   thrombolytic activities; receptor or ligand activities; or may be
CC   involved in oncogenesis, cancer cell proliferation or metastasis.
CC   Depending on their biological activities, polypeptides and nucleotides of
CC   the invention are useful for preventing, treating or ameliorating medical
CC   conditions, e.g., by protein or gene therapy. Such conditions include
CC   cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC   disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC   proliferative retinopathy, atherosclerosis, coronary heart disease,
CC   arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC   vascular growth. Polypeptides involved with tissue regeneration and
CC   repair (or nucleic acids encoding them) may be used to promote wound
CC   healing (e.g., of burns, incisions and ulcers), while those with
CC   immunomodulatory activities may be used in the treatment of viral,
CC   bacterial and fungal infections in addition to immune disorders.
CC   Polypeptides with growth factor activity may be used in cell cultures to
CC   promote cell growth. For example, such polypeptides may be used to
CC   manipulate stem cells in culture to give rise to neuroepithelial cells
CC   that can be used to augment or replace cells damaged by illness,
CC   autoimmune disease or accidental damage. The polypeptides and nucleotides
CC   may also be used in the diagnosis of the above conditions, and in drug
CC   screening techniques. The present sequence represents a novel human
CC   polypeptide of the invention
XX
SQ   Sequence 431 AA;

  Query Match             43.7%;  Score 181;  DB 4;  Length 431;
  Best Local Similarity   100.0%;  Pred. No. 7e-168;
  Matches  181;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         18 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 77

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 137

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 197

Qy        181 I 181
              |
Db        198 I 198
```

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RESULT 11
AAM79882
ID   AAM79882 standard; protein; 431 AA.
XX
AC   AAM79882;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human protein SEQ ID NO 3528.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US004098.
XX
PR   03-FEB-2000; 2000US-00496914.
PR   27-APR-2000; 2000US-00560875.
PR   20-JUN-2000; 2000US-00598075.
PR   19-JUL-2000; 2000US-00620325.
PR   01-SEP-2000; 2000US-00654936.
PR   15-SEP-2000; 2000US-00663561.
PR   20-OCT-2000; 2000US-00693325.
PR   30-NOV-2000; 2000US-00728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y;
PI   Ma Y,  Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   N-PSDB; AAK53015.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT   in diagnosis and gene therapy.
XX
PS   Claim 20; Page 371; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC   (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC   sequence listing were missing at the time of publication
XX
SQ   Sequence 431 AA;

  Query Match             43.7%;  Score 181;  DB 4;  Length 431;
  Best Local Similarity   100.0%;  Pred. No. 7e-168;
  Matches  181;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         18 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 77

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db          78 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 137

Qy         121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         138 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 197

Qy         181 I 181
               |
Db         198 I 198


RESULT 12
AAM70426
ID   AAM70426 standard; protein; 140 AA.
XX
AC   AAM70426;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human bone marrow expressed probe encoded protein SEQ ID NO: 30732.
XX
KW   Human; bone marrow expressed exon; gene expression analysis; probe;
KW   microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS   Homo sapiens.
XX
PN   WO200157276-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000668.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488900/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for analyzing
PT   gene expression in human bone marrow.
XX
PS   Example 4; SEQ ID NO 30732; 658pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   bone marrow. They can be used to measure gene expression in bone marrow
CC   samples, which may enable the improved diagnosis and treatment of cancers
CC   such as lymphoma, leukaemia and myeloma. The present sequence is a
CC   protein encoded by one of the probes of the invention
XX
SQ   Sequence 140 AA;

  Query Match             31.2%;  Score 129;  DB 4;  Length 140;
  Best Local Similarity   100.0%;  Pred. No. 2e-117;
  Matches  129;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          83 FSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLFIDQ 142
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 FSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLFIDQ 60

Qy         143 RLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPGTVM 202
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 RLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPGTVM 120

Qy         203 LLANYIFFR 211
               |||||||||
Db         121 LLANYIFFR 129


Search completed: March 31, 2006, 10:02:29
Job time : 224.573 secs
```

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 10:02:58 ; Search time 26.0989 Seconds
(without alignments)
1526.262 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 414
Sequence: 1 MNPTLGLAIFLAVLLTVKGL.....YSEKIPSVLFLGKIVNPIGK 414

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 15

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description

No matches found

Search completed: March 31, 2006, 10:08:39
Job time : 26.0989 secs

OM protein - protein search, using sw model

Run on: March 31, 2006, 09:55:21 ; Search time 157.105 Seconds
(without alignments)
1859.193 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 414
Sequence: 1 MNPTLGLAIFLAVLLTVKGL.....YSEKIPSVLFLGKIVNPIGK 414

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 15

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	414	100.0	414	2	Q8IW75_HUMAN	Q8iw75 homo sapien
2	19	4.6	413	2	Q7TMF5_MOUSE	Q7tmf5 mus musculu
3	19	4.6	413	2	Q9CQ32_MOUSE	Q9cq32 m mus muscu
4	19	4.6	413	2	Q6P6M3_MOUSE	Q6p6m3 mus musculu
5	16	3.9	411	2	Q8R4Z1_RAT	Q8r4z1 rattus norv

ALIGNMENTS

RESULT 1
Q8IW75_HUMAN
ID Q8IW75_HUMAN PRELIMINARY; PRT; 414 AA.
AC Q8IW75;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Serine (Or cysteine) proteinase inhibitor, clade A (Alpha-1
DE antiproteinase, antitrypsin), member 12 (OL-64) (Visceral adipose-
DE specific SERPIN).
GN Name=SERPINA12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RG NIH MGC Project;
RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RA Chen S., Guo J.H., Yu L.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Hida K., Wada J., Zhang H.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Belongs to the serpin family.
DR EMBL; BC040857; AAH40857.1; -; mRNA.
DR EMBL; AY177692; AAO18649.1; -; mRNA.
DR EMBL; AY326420; AAP88384.1; -; mRNA.
DR HSSP; P01009; 1QMB.
DR Ensembl; ENSG00000165953; Homo sapiens.
DR HGNC; HGNC:18359; SERPINA12.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
KW Serpin.
SQ SEQUENCE 414 AA; 47175 MW; 5C70F1AB5935661C CRC64;

Query Match 100.0%; Score 414; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
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Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
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Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 2
Q7TMF5_MOUSE
ID   Q7TMF5_MOUSE PRELIMINARY;      PRT;   413 AA.
AC   Q7TMF5;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Visceral adipose-specific SERPIN.
GN   Name=Serpina12;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Swiss Webster;
RA   Hida K., Wada J., Zhang H.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the serpin family.
DR   EMBL; AY326419; AAP88383.1; -; mRNA.
DR   HSSP; P01008; 1ATH.
DR   MGI; MGI:1915304; Serpina12.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR000295; Prot_inh_Lserp2.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   Pfam; PF00079; Serpin; 1.
DR   PRINTS; PR00780; LEUSERPINII.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Serpin.
SQ   SEQUENCE   413 AA;  47674 MW;  EE2B3B08C2DD418F CRC64;

  Query Match             4.6%;  Score 19;  DB 2;  Length 413;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-10;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        344 HRSLKVGEAVHKAELKMDE 362
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Db        344 HRSLKVGEAVHKAELKMDE 362


RESULT 3
Q9CQ32_MOUSE
ID   Q9CQ32_MOUSE PRELIMINARY;      PRT;   413 AA.
AC   Q9CQ32;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched
DE   library, clone:4632419J12 product:hypothetical Serpins containing
DE   protein, full insert sequence (Mus musculus 17 days embryo head cDNA,
DE   RIKEN full-length enriched library, clone:3300001F13
DE   product:hypothetical Serpins containing protein, full insert
DE   sequence).
GN   Name=Serpina12;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
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RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the serpin family.
DR   EMBL; AK014589; BAB29447.1; -; mRNA.
DR   EMBL; AK014346; BAB29287.1; -; mRNA.
DR   HSSP; P01008; 1ATH.
DR   Ensembl; ENSMUSG00000041567; Mus musculus.
DR   MGI; MGI:1915304; Serpina12.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR000295; Prot_inh_Lserp2.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   Pfam; PF00079; Serpin; 1.
DR   PRINTS; PR00780; LEUSERPINII.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Hypothetical protein; Serpin.
SQ   SEQUENCE   413 AA;  47634 MW;  D0AE8E1EE24FD60A CRC64;

  Query Match             4.6%;  Score 19;  DB 2;  Length 413;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-10;
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Qy        344 HRSLKVGEAVHKAELKMDE 362
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Db        344 HRSLKVGEAVHKAELKMDE 362


RESULT 4
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ID   Q6P6M3_MOUSE PRELIMINARY;      PRT;   413 AA.
AC   Q6P6M3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Visceral adipose-specific SERPIN.
GN   Name=Serpina12;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Jaw and Limb;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Jaw and Limb;
RG   NIH MGC Project;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the serpin family.
DR   EMBL; BC062143; AAH62143.1; -; mRNA.
DR   HSSP; P01008; 1ATH.
DR   Ensembl; ENSMUSG00000041567; Mus musculus.
DR   MGI; MGI:1915304; Serpina12.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR000295; Prot_inh_Lserp2.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   Pfam; PF00079; Serpin; 1.
DR   PRINTS; PR00780; LEUSERPINII.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW   Serpin.
SQ   SEQUENCE   413 AA;  47630 MW;  CE1940BA2EE35811 CRC64;

  Query Match             4.6%;  Score 19;  DB 2;  Length 413;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-10;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        344 HRSLKVGEAVHKAELKMDE 362
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Db        344 HRSLKVGEAVHKAELKMDE 362


RESULT 5
Q8R4Z1_RAT
ID   Q8R4Z1_RAT  PRELIMINARY;      PRT;   411 AA.
AC   Q8R4Z1;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Visceral adipose tissue specific SERPIN.
GN   Name=Serpina12; Synonyms=Vaspin;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=OLETF; TISSUE=Visceral adipose;
RA   Hida K., Wada J., Zhang H., Shikata K., Makino H.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the serpin family.
DR   EMBL; AF245398; AAL99574.1; -; mRNA.
DR   HSSP; P01008; 1ATH.
DR   Ensembl; ENSRNOG00000009710; Rattus norvegicus.
DR   RGD; 708485; Serpina12.
DR   GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR   InterPro; IPR000295; Prot_inh_Lserp2.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   Pfam; PF00079; Serpin; 1.
DR   PRINTS; PR00780; LEUSERPINII.
DR   SMART; SM00093; SERPIN; 1.
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KW   Serpin.
SQ   SEQUENCE   411 AA;  47527 MW;  29FA271FF8CC8A2D CRC64;

  Query Match             3.9%;  Score 16;  DB 2;  Length 411;
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Qy         71 NIFLSPLSISTAFSML 86
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Db         71 NIFLSPLSISTAFSML 86


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Job time : 159.105 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

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Title: US-10-664-356-1562
Perfect score: 414
Sequence: 1 MNPTLGLAIFLAVLLTVKGL.....YSEKIPSVLFLGKIVNPIGK 414

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

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Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0
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Post-processing: Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	414	100.0	414	2	US-09-755-665-14	Sequence 14, Appl
2	414	100.0	414	2	US-09-755-665-55	Sequence 55, Appl
3	414	100.0	414	2	US-09-755-665-56	Sequence 56, Appl
4	414	100.0	415	2	US-09-461-325-134	Sequence 134, App
5	414	100.0	415	2	US-10-012-542-134	Sequence 134, App
6	414	100.0	415	2	US-10-115-123-134	Sequence 134, App
7	310	74.9	361	2	US-09-755-665-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1
US-09-755-665-14
; Sequence 14, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Taillon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-14

Query Match 100.0%; Score 414; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
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Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
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Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
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RESULT 2
US-09-755-665-55
; Sequence 55, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Taillon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-55

Query Match 100.0%; Score 414; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
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Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
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RESULT 3
US-09-755-665-56
; Sequence 56, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Taillon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-56

Query Match 100.0%; Score 414; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
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RESULT 4
US-09-461-325-134
; Sequence 134, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: PZ029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (415)
; OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring L-amino acids
US-09-461-325-134

Query Match 100.0%; Score 414; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
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Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 5
US-10-012-542-134
; Sequence 134, Application US/10012542
; Patent No. 6627741
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029P1
;  CURRENT APPLICATION NUMBER: US/10/012,542
;  CURRENT FILING DATE:  2001-12-12
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
;   LENGTH: 415
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (415)
;   OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring L-amino
;   OTHER INFORMATION: acids
US-10-012-542-134

  Query Match            100.0%;  Score 414;  DB 2;  Length 415;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 6
US-10-115-123-134
; Sequence 134, Application US/10115123
; Patent No. 6774216
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029G30AP1D2
;  CURRENT APPLICATION NUMBER: US/10/115,123
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: PCT/US99/13418
;  PRIOR FILING DATE: 1999-06-15
;  PRIOR APPLICATION NUMBER: 60/089,507
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,508
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,509
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,510
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/090,112
;  PRIOR FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: 60/090,113
;  PRIOR FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
;   LENGTH: 415
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (415)
;   OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring L-amino acids
US-10-115-123-134

  Query Match            100.0%;  Score 414;  DB 2;  Length 415;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
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RESULT 7
US-09-755-665-57
; Sequence 57, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
;  APPLICANT: Prayaga, Sudhirdas K.
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Taillon, Bruce E.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  MacDougall, John
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-631
;  CURRENT APPLICATION NUMBER: US/09/755,665
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
;   LENGTH: 361
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)..(361)
;   OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
;   OTHER INFORMATION: specification
US-09-755-665-57

  Query Match            74.9%;  Score 310;  DB 2;  Length 361;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-292;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLH 113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLH 60

Qy        114 EGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMA 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMA 120

Qy        174 QKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKN 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKN 180

Qy        234 SSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFS 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFS 240

Qy        294 RWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 RWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 300

Qy        354 HKAELKMDER 363
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Db        301 HKAELKMDER 310


Search completed: March 31, 2006, 10:09:51
Job time : 33.775 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 10:08:54 ; Search time 120.26 Seconds
(without alignments)
1438.400 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 414
Sequence: 1 MNPTLGLAIFLAVLLTVKGL.....YSEKIPSVLFLGKIVNPIGK 414

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

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Total number of hits satisfying chosen parameters: 14

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : Published_Applications_AA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	414	100.0	414	3	US-09-755-665-14	Sequence 14, Appl
2	414	100.0	414	3	US-09-755-665-55	Sequence 55, Appl
3	414	100.0	414	3	US-09-755-665-56	Sequence 56, Appl
4	414	100.0	414	4	US-10-168-425-12	Sequence 12, Appl
5	414	100.0	414	4	US-10-629-248-14	Sequence 14, Appl
6	414	100.0	414	4	US-10-629-248-55	Sequence 55, Appl
7	414	100.0	414	4	US-10-629-248-56	Sequence 56, Appl
8	414	100.0	415	4	US-10-012-542-134	Sequence 134, App
9	414	100.0	415	4	US-10-115-123-134	Sequence 134, App
10	414	100.0	415	4	US-10-800-834-134	Sequence 134, App
11	310	74.9	361	3	US-09-755-665-57	Sequence 57, Appl
12	310	74.9	361	4	US-10-629-248-57	Sequence 57, Appl
13	181	43.7	431	4	US-10-276-774-2202	Sequence 2202, Ap
14	129	31.2	140	3	US-09-864-761-48438	Sequence 48438, A

ALIGNMENTS

RESULT 1
US-09-755-665-14
; Sequence 14, Application US/09755665
; Patent No. US20020107186A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Taillon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-14

Query Match 100.0%; Score 414; DB 3; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
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Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
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RESULT 2
US-09-755-665-55
; Sequence 55, Application US/09755665
; Patent No. US20020107186A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Taillon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-755-665-55

Query Match 100.0%; Score 414; DB 3; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
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Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
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Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
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Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
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RESULT 3
US-09-755-665-56
; Sequence 56, Application US/09755665
; Patent No. US20020107186A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Taillon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-56

Query Match 100.0%; Score 414; DB 3; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
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Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
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Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
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Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
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RESULT 4
US-10-168-425-12
; Sequence 12, Application US/10168425
; Publication No. US20030124706A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YANG, Junming
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BURFORD, Neil
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: REDDY, Roopa
; APPLICANT: YUE, Henry
; APPLICANT: NGUYEN, Danniel B.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YAO, Monique G.
; APPLICANT: LAL, Preeti
; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: PI-0003 PCT
; CURRENT APPLICATION NUMBER: US/10/168,425
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/172,055; 60/177,334; 60/178,884; 60/179,903
; PRIOR FILING DATE: 1999-12-23; 2000-01-21; 2000-01-28; 2000-02-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030124706A1 7257324CD1
US-10-168-425-12

Query Match 100.0%; Score 414; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
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Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
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Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
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Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 5
US-10-629-248-14
; Sequence 14, Application US/10629248
; Publication No. US20040116671A1
; GENERAL INFORMATION:
;  APPLICANT: Prayaga, Sudhirdas K.
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Taillon, Bruce E.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  MacDougall, John
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-631
;  CURRENT APPLICATION NUMBER: US/10/629,248
;  CURRENT FILING DATE:  2003-07-28
;  PRIOR APPLICATION NUMBER: US/09/755,665
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 414
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-629-248-14

  Query Match           100.0%;  Score 414;  DB 4;  Length 414;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
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Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 6
US-10-629-248-55
; Sequence 55, Application US/10629248
; Publication No. US20040116671A1
; GENERAL INFORMATION:
;  APPLICANT: Prayaga, Sudhirdas K.
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Taillon, Bruce E.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  MacDougall, John
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-631
;  CURRENT APPLICATION NUMBER: US/10/629,248
;  CURRENT FILING DATE:  2003-07-28
;  PRIOR APPLICATION NUMBER: US/09/755,665
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
;   LENGTH: 414
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-629-248-55

  Query Match           100.0%;  Score 414;  DB 4;  Length 414;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
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Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 7
US-10-629-248-56
; Sequence 56, Application US/10629248
; Publication No. US20040116671A1
; GENERAL INFORMATION:
;  APPLICANT: Prayaga, Sudhirdas K.
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Taillon, Bruce E.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  MacDougall, John
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
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;  FILE REFERENCE: 15966-631
;  CURRENT APPLICATION NUMBER: US/10/629,248
;  CURRENT FILING DATE:  2003-07-28
;  PRIOR APPLICATION NUMBER: US/09/755,665
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
;   LENGTH: 414
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-629-248-56

  Query Match             100.0%;  Score 414;  DB 4;  Length 414;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 8
US-10-012-542-134
; Sequence 134, Application US/10012542
; Publication No. US20030044851A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029P1
;  CURRENT APPLICATION NUMBER: US/10/012,542
;  CURRENT FILING DATE:  2001-12-12
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
;   LENGTH: 415
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (415)
;   OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring L-amino
;   OTHER INFORMATION: acids
US-10-012-542-134

  Query Match             100.0%;  Score 414;  DB 4;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 9
US-10-115-123-134
; Sequence 134, Application US/10115123
; Publication No. US20030065151A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029G30AP1D2
;  CURRENT APPLICATION NUMBER: US/10/115,123
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: PCT/US99/13418
;  PRIOR FILING DATE: 1999-06-15
;  PRIOR APPLICATION NUMBER: 60/089,507
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,508
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,509
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,510
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/090,112
;  PRIOR FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: 60/090,113
;  PRIOR FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
;   LENGTH: 415
```

```
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (415)
;   OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring L-amino acids
US-10-115-123-134

  Query Match           100.0%;  Score 414;  DB 4;  Length 415;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 10
US-10-800-834-134
; Sequence 134, Application US/10800834
; Publication No. US20040146930A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029P1D3
;  CURRENT APPLICATION NUMBER: US/10/800,834
;  CURRENT FILING DATE:  2004-03-16
;  PRIOR APPLICATION NUMBER: 10/115,123
;  PRIOR FILING DATE: 2002-04-04
;  PRIOR APPLICATION NUMBER: 09/461,325
;  PRIOR FILING DATE: 1999-12-14
;  PRIOR APPLICATION NUMBER: PCT/US99/13418
;  PRIOR FILING DATE: 1999-06-15
;  PRIOR APPLICATION NUMBER: 60/089,507
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,508
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,509
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,510
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/090,112
;  PRIOR FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: 60/090,113
;  PRIOR FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
;   LENGTH: 415
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (415)
;   OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring L-amino acids
US-10-800-834-134

  Query Match           100.0%;  Score 414;  DB 4;  Length 415;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180

Qy        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPM 240

Qy        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLS 300

Qy        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKM 360

Qy        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DERGTEGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 11
US-09-755-665-57
; Sequence 57, Application US/09755665
; Patent No. US20020107186A1
; GENERAL INFORMATION:
;  APPLICANT: Prayaga, Sudhirdas K.
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Taillon, Bruce E.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  MacDougall, John
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-631
;  CURRENT APPLICATION NUMBER: US/09/755,665
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
;   LENGTH: 361
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)..(361)
;   OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
;   OTHER INFORMATION: specification
US-09-755-665-57

  Query Match            74.9%;  Score 310;  DB 3;  Length 361;
  Best Local Similarity  100.0%;  Pred. No. 4.2e-291;
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  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLH 113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLH 60

Qy        114 EGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMA 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMA 120

Qy        174 QKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKN 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKN 180

Qy        234 SSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFS 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFS 240

Qy        294 RWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 RWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 300

Qy        354 HKAELKMDER 363
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Db        301 HKAELKMDER 310


RESULT 12
US-10-629-248-57
; Sequence 57, Application US/10629248
; Publication No. US20040116671A1
; GENERAL INFORMATION:
;  APPLICANT: Prayaga, Sudhirdas K.
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Taillon, Bruce E.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  MacDougall, John
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-631
;  CURRENT APPLICATION NUMBER: US/10/629,248
;  CURRENT FILING DATE:  2003-07-28
;  PRIOR APPLICATION NUMBER: US/09/755,665
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
;   LENGTH: 361
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)..(361)
;   OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
;   OTHER INFORMATION: specification
US-10-629-248-57

  Query Match            74.9%;  Score 310;  DB 4;  Length 361;
  Best Local Similarity  100.0%;  Pred. No. 4.2e-291;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         54 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLH 113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLH 60

Qy        114 EGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMA 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMA 120

Qy        174 QKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKN 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKN 180

Qy        234 SSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFS 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFS 240

Qy        294 RWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 RWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 300

Qy        354 HKAELKMDER 363
              ||||||||||
Db        301 HKAELKMDER 310


RESULT 13
US-10-276-774-2202
; Sequence 2202, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  APPLICANT:  Tang, Y, Tom et al
;  TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
;  FILE REFERENCE: 21272-030
;  CURRENT APPLICATION NUMBER: US/10/276,774
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 09/560,875
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 09/496,914
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 2700
;  SOFTWARE: Custom
; SEQ ID NO 2202
;   LENGTH: 431
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-276-774-2202

  Query Match            43.7%;  Score 181;  DB 4;  Length 431;
  Best Local Similarity  100.0%;  Pred. No. 3.8e-166;
  Matches  181;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         18 MNPTLGLAIFLAVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLL 77

Qy         61 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 KKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYII 137

Qy        121 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 HELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDF 197

Qy        181 I 181
              |
Db        198 I 198


RESULT 14
US-09-864-761-48438
; Sequence 48438, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
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;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48438
;   LENGTH: 140
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AL132708.1
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
;   OTHER INFORMATION: SWISSPROT HIT: P50447, EVALUE 8.00e-28
;   OTHER INFORMATION: EST_HUMAN HIT: AV649144.1, EVALUE 3.00e-27
US-09-864-761-48438

  Query Match             31.2%;  Score 129;  DB 3;  Length 140;
  Best Local Similarity   100.0%;  Pred. No. 3e-116;
  Matches  129;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          83 FSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLFIDQ 142
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 FSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLFIDQ 60

Qy         143 RLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPGTVM 202
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 RLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPGTVM 120

Qy         203 LLANYIFFR 211
               |||||||||
Db         121 LLANYIFFR 129


Search completed: March 31, 2006, 10:13:53
Job time : 121.26 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 10:10:05 ; Search time 16.8875 Seconds
(without alignments)
746.288 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 414
Sequence: 1 MNPTLGLAIFLAVLLTVKGL.....YSEKIPSVLFLGKIVNPIGK 414

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 180808 seqs, 30441898 residues

Word size : 15

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

No matches found

Search completed: March 31, 2006, 10:14:30
Job time : 16.8875 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 09:54:55 ; Search time 210.927 Seconds
(without alignments)
822.818 Million cell updates/sec

Title: US-10-664-356-1562_COPY_20_414
Perfect score: 395
Sequence: 1 LLKPSFSPRNYKALSEVQGW.....YSEKIPSVLFLGKIVNPIGK 395

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word-size: 15

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	395	100.0	414	4	AAU05754	Aau05754 Human NOV
2	395	100.0	414	4	AAE04885	Aae04885 Human pro
3	395	100.0	414	6	ADA57300	Ada57300 Human sec
4	395	100.0	414	6	ADA41179	Ada41179 Human sec
5	395	100.0	414	8	ADN05952	Adn05952 Antipsori
6	395	100.0	415	3	AAY86217	Aay86217 Human sec
7	395	100.0	415	6	ABO53360	Abo53360 Novel hum
8	334	84.6	414	4	AAM78898	Aam78898 Human pro
9	310	78.5	358	4	AAU05759	Aau05759 Human NOV
10	170	43.0	431	4	ABB11832	Abb11832 Human sec
11	170	43.0	431	4	AAM79882	Aam79882 Human pro
12	129	32.7	140	4	AAM70426	Aam70426 Human bon

ALIGNMENTS

RESULT 1
AAU05754
ID AAU05754 standard; protein; 414 AA.
XX
AC AAU05754;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human NOV7 polypeptide.
XX
KW Human; NOV7; AL132990 B; fertility disorder; spermatogenesis; cardiant;
KW cytostatic; immunomodulatory; antiproliferative; antidiabetic;
KW cell proliferation; cancer; diabetic retinopathy; angiogenic disorder;
KW pulmonary disorder; haematopoietic disorder; immunological disorder;
KW inflammatory disorder; tumour related disorders; emphysema; cirrhosis;
KW wound healing; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200149729-A2.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000299.
XX
PR 06-JAN-2000; 2000US-0174724P.
PR 11-JAN-2000; 2000US-0175434P.
PR 11-JAN-2000; 2000US-0175488P.
PR 12-JAN-2000; 2000US-0175696P.
PR 12-JAN-2000; 2000US-0175743P.
PR 13-JAN-2000; 2000US-0175819P.
PR 07-AUG-2000; 2000US-0223524P.
PR 04-JAN-2001; 2001US-00755665.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Prayaga SK, Majumder K, Taillon BE, Spaderna SK, Spytek KA;
PI Macdougall J;
XX
DR WPI; 2001-418356/44.
DR N-PSDB; AAS10874.
XX
PT Nucleic acids encoding polypeptides, designated NOVX polypeptides, useful
PT for treating a syndrome associated with a NOVX-associated disorder, e.g.
PT cell proliferation (e.g. cancer and diabetic retinopathy), angiogenic or
PT pulmonary disorder.
XX
PS Claim 1; Page 32; 144pp; English.
XX
CC The invention relates to nucleic acids encoding NOVX (X being an integer
CC from 1-8) polypeptides. The NOVX nucleic acids and polypeptides are
CC useful in diagnosing, treating or manufacturing a medicament for a
CC disease or disorder associated with NOVX e.g. cell proliferation (cancer
CC and diabetic retinopathy), angiogenic or pulmonary disorders, fertility
CC disorders (e.g of spermatogenesis), haematopoietic, immunological,
CC inflammatory and tumour related disorders, emphysema, cirrhosis, wound
CC healing. NOVX nucleic acids are also useful in gene therapy. They are
CC also used for screening for a modulator of activity or of latency or
CC predisposition to a NOVX-associated disorder. They are also useful for
CC determining the presence of or predisposition to a NOVX-associated
CC disorder. The present sequence represents NOV7 (AL132990 B), which has
CC sequence homology to an unidentified human secreted protein (HWHGUS54)
CC and to alpha1 anti-trypsin
XX
SQ Sequence 414 AA;

Query Match 100.0%; Score 395; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 79

Qy         61 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 139

Qy        121 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        140 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 199

Qy        181 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 259

Qy        241 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 319

Qy        301 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 379

Qy        361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 395
              ||||||||||||||||||||||||||||||||||||
Db        380 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 2
AAE04885
ID   AAE04885 standard; protein; 414 AA.
XX
AC   AAE04885;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human protease protein-12 (PRTS-12).
XX
KW   Human; protease protein-12; PRTS-12; cytostatic; hypotensive; antiviral;
KW   gastrointestinal disorder; anorexia; dysphagia; cardiovascular disorder;
KW   atherosclerosis; vasculitis; autoimmune disorder; inflammatory disorder;
KW   Alzheimer's disease; cell proliferative disorder; dermatitis; cirrhosis;
KW   acquired immune deficiency syndrome; AIDS; neurological disorder; asthma;
KW   developmental disorder; epithelial disorder; eczema; dementia; nootropic;
KW   neurological disorder; reproductive disorder; infertility; teratogenesis;
KW   immunosuppressive; drug screening; actinic keratosis; cardiant; epilepsy;
KW   anaemia; antitumour; gene therapy; antibacterial.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Signal_peptide
FT   Protein         20. .414
FT                   /note= "Mature human PRTS-12"
XX
PN   WO200146443-A2.
XX
PD   28-JUN-2001.
XX
PF   19-DEC-2000; 2000WO-US034811.
XX
PR   23-DEC-1999;   99US-0172055P.
PR   21-JAN-2000; 2000US-0177334P.
PR   28-JAN-2000; 2000US-0178884P.
PR   02-FEB-2000; 2000US-0179903P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Yang J,  Baughn MR,  Burford N,  Au-Young J,  Lu DAM,  Reddy R;
PI   Yue H,  Nguyen DB,  Tang YT,  Yao MG,  Lal P;
XX
DR   WPI; 2001-418080/44.
DR   N-PSDB; AAD09549.
XX
PT   Novel human protease proteins (PRTS) useful for diagnosing, treating,
PT   preventing gastrointestinal, cardiovascular, autoimmune/inflammatory,
PT   cell proliferative disorders associated with abnormal expression of PRTS.
XX
PS   Claim 1; Page 118; 129pp; English.
XX
CC   The present sequence is human protease protein (PRTS-12). Human PRTS and
CC   its nucleic acid molecule are useful for the diagnosis, treatment and
CC   prevention of disorders associated with increased or decreased expression
CC   of PRTS. Examples of such disorders include, gastrointestinal disorder
CC   such as anorexia, dysphagia; cardiovascular disorder such as
CC   atherosclerosis, vasculitis; autoimmune/inflammatory disorder such as
CC   acquired immune deficiency syndrome (AIDS), asthma; cell proliferative
CC   disorder such as actinic keratosis, cirrhosis; developmental disorder
CC   such as epilepsy, anaemia; epithelial disorder such as allergic contact
CC   dermatitis, eczema; neurological disorder such as Alzheimer's disease,
CC   dementia and reproductive disorder such as infertility and teratogenesis.
CC   PRTS DNA is useful for creating 'knockin' humanised animals (pigs) or
CC   transgenic animals (mice or rats) to model human disease. PRTS DNA is
CC   also in useful is gene therapy. PRTS and its immunogenic fragments are
CC   useful for screening libraries of compounds in several drug screening
CC   assays. PRTS is useful for analysing the proteome of a tissue or cell
CC   type
XX
SQ   Sequence 414 AA;

  Query Match             100.0%;  Score 395;  DB 4;  Length 414;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  395;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 79

Qy         61 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 139

Qy        121 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 199

Qy        181 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 259

Qy        241 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 319

Qy        301 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 379

Qy        361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 395
              ||||||||||||||||||||||||||||||||||||
Db        380 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 3
ADA57300
ID   ADA57300 standard; protein; 414 AA.
XX
AC   ADA57300;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human secreted protein #583.
XX
KW   immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW   cytostatic; cerebroprotective; neuroprotective; nootropic;
KW   cardiovascular; antiarteriosclerotic; gene therapy;
KW   human secreted protein; immune disorder; inflammation;
KW   respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW   inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW   multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW   Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW   triple helix formation; antisense gene therapy; forensic biology.
XX
OS   Homo sapiens.
```

XX
PN WO2002102994-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008278.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-167512/16.
DR N-PSDB; ADA56404.
XX
PT New human secreted polypeptides and polynucleotides, useful for
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT conditions, respiratory disorders, cancers, CNS disorders, or
PT neurodegenerative disorders.
XX
PS Claim 13; SEQ ID NO 1490; 1754pp; English.
XX
CC The invention relates to 592 new human secreted polypeptides useful for
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC conditions, respiratory disorders, cancers, CNS disorders, or
CC neurodegenerative disorders, or polypeptides comprising an amino acid
CC sequence at least 95% identical to the new sequences. The polypeptides,
CC antibodies or antibody fragments that bind to the polypeptides, nucleic
CC acids encoding the polypeptides, agonists or antagonists that binds to
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC compositions for diagnosing, treating or preventing an e.g. immune
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC polynucleotides are useful for chromosome identification, chromosome
CC mapping, for controlling gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy, for identifying individuals
CC from minute biological samples, in forensic biology, and as hybridization
CC probes. The polypeptides are useful for as molecular weight markers on
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC gels, to raise antibodies, for testing biological activities, and for
CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to one of the polypeptide of the invention. Note: The sequence data for
CC this patent did form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 414 AA;

Query Match 100.0%; Score 395; DB 6; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 79

Qy         61 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 139

Qy        121 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 199

Qy        181 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 259

Qy        241 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 319

Qy        301 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 379

Qy        361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 395
              ||||||||||||||||||||||||||||||||||||
Db        380 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
```

RESULT 4
ADA41179
ID ADA41179 standard; protein; 414 AA.
XX
AC ADA41179;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted protein.
XX
KW Human; secreted protein; cancer; hyperproliferative disorder;
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW vulnerary; cardiant; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2002102993-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008123.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-175238/17.
XX
PT New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing,
PT preventing or treating cancer or other hyperproliferative disorder,
PT asthma, allergies or AIDS.
XX
PS Claim 1; SEQ ID NO 1561; 3205pp; English.
XX
CC The invention relates to novel genes ADA39629-ADA40565 and proteins
CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
CC treating or ameliorating medical conditions e.g. by protein or gene
CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
CC fragments, and agonists or antagonists that bind to the polypeptide are
CC useful for preparing a diagnostic or pharmaceutical composition for
CC diagnosing or treating cancer or other hyperproliferative disorder. The
CC polypeptides and nucleic acid molecules are also useful for detecting,
CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
CC or other hyperproliferative disorders including neoplasms, autoimmune
CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
CC thrombocytopenia), allergic reactions including asthma or eczema,

```
CC   inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC   bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC   Alzheimer's disease or Parkinson's disease), cardiovascular disorders
CC   (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
CC   fungal or viral infections including HIV/AIDS), or wound healing and
CC   disorders of epithelial cell proliferation. The nucleic acids are also
CC   useful for chromosome identification, radiation hybrid mapping or long-
CC   range restriction mapping, as molecular weight markers, or as
CC   hybridization or diagnostic probes. The polypeptides and antibodies are
CC   useful for providing immunological probes for differential identification
CC   of the tissues immunohistochemistry assays. Note: The sequence data for
CC   this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 414 AA;

  Query Match           100.0%;  Score 395;  DB 6;  Length 414;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  395;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 79

Qy         61 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 139

Qy        121 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 199

Qy        181 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 259

Qy        241 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 319

Qy        301 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 379

Qy        361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 395
              |||||||||||||||||||||||||||||||||||
Db        380 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 5
ADN05952
ID   ADN05952 standard; protein; 414 AA.
XX
AC   ADN05952;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Antipsoriatic protein sequence #1136.
XX
KW   antipsoriatic; gene therapy; psoriasis; diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO2004028479-A2.
XX
PD   08-APR-2004.
XX
PF   25-SEP-2003; 2003WO-US030907.
XX
PR   25-SEP-2002; 2002US-0414006P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI   Wu TD;
XX
DR   WPI; 2004-305105/28.
DR   N-PSDB; ADN05951.
XX
PT   New PRO nucleic acid or polypeptide, useful for preparing a
PT   pharmaceutical composition for diagnosing or treating psoriasis in a
PT   mammal.
XX
PS   Claim 9; SEQ ID NO 2347; 3069pp; English.
XX
CC   The invention relates to novel polynucleotide and polypeptides for
CC   treating psoriasis or a sequence having at least 80% identity to the
CC   above sequences. The nucleic acid is useful for preparing a composition
CC   for diagnosing or treating psoriasis in a mammal. This sequence
CC   corresponds to one of the polypeptides of the invention.
XX
SQ   Sequence 414 AA;

  Query Match           100.0%;  Score 395;  DB 8;  Length 414;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  395;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 79

Qy         61 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 139

Qy        121 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 199

Qy        181 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 259

Qy        241 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 319

Qy        301 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 379

Qy        361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 395
              |||||||||||||||||||||||||||||||||||
Db        380 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 6
AAY86217
ID   AAY86217 standard; protein; 415 AA.
XX
AC   AAY86217;
XX
DT   19-APR-2000  (first entry)
XX
DE   Human secreted protein HWHGU54, SEQ ID NO:132.
XX
KW   Human; secreted protein; cancer; tumour; developmental abnormality;
KW   foetal deficiency; blood disorder; immune system disorder; inflammation;
KW   autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW   schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW   atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW   digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
KW   therapy.
XX
OS   Homo sapiens.
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XX
PN   WO9966041-A1.
XX
PD   23-DEC-1999.
XX
PF   15-JUN-1999;   99WO-US013418.
XX
PR   16-JUN-1998;   98US-0089507P.
PR   16-JUN-1998;   98US-0089508P.
PR   16-JUN-1998;   98US-0089509P.
PR   16-JUN-1998;   98US-0089510P.
PR   22-JUN-1998;   98US-0090112P.
PR   22-JUN-1998;   98US-0090113P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Ni J, Rosen CA, Wei Y, Young PE, Florence KA;
PI   Soppet DR, Brewer LA, Endress GA, Carter KC, Mucenski M, Ebner R;
PI   Lafleur DW, Olsen HS, Shi Y, Moore PA, Komatsoulis G;
XX
DR   WPI; 2000-106100/09.
DR   N-PSDB; AAZ97021.
XX
PT   New isolated human genes and the secreted polypeptides they encode,
PT   useful for diagnosis and treatment of e.g. cancers, neurological
PT   disorders, immune diseases, inflammation or blood disorders.
XX
PS   Claim 1; Page 389-390; 586pp; English.
XX
CC   AAZ97019 to AAZ97137 represent 94 isolated human secreted protein genes.
CC   AAY86215 to AAY86333 are the secreted proteins encoded by the 94 human
CC   genes. This sequence represents a fragment of one of the human secreted
CC   proteins. The genes and their corresponding secreted polypeptides are
CC   useful for preventing, treating or ameliorating medical conditions, e.g.,
CC   by protein or gene therapy. Also pathological conditions can be diagnosed
CC   by determining the amount of the new polypeptides in a sample or by
CC   determining the presence of mutations in the new genes. Specific uses are
CC   described for each of the 94 genes, based on which tissues they are most
CC   highly expressed in, and include developing products for the diagnosis or
CC   treatment of cancer, tumours, developmental abnormalities and foetal
CC   deficiencies, blood disorders, diseases of the immune system, autoimmune
CC   diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
CC   schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
CC   atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
CC   digestive/endocrine disorders, infections and AIDS. The polypeptides are
CC   also useful for identifying their binding partners. The sequences shown
CC   in AAY86334 to AAY86585 represent fragments of the secreted proteins
XX
SQ   Sequence 415 AA;

  Query Match             100.0%;  Score 395;  DB 3;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  395;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 79

Qy         61 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 139

Qy        121 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 199

Qy        181 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 259

Qy        241 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 319

Qy        301 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 379

Qy        361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 395
              |||||||||||||||||||||||||||||||||||
Db        380 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 7
ABO53360
ID   ABO53360 standard; protein; 415 AA.
XX
AC   ABO53360;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Novel human secreted protein #3.
XX
KW   Human; vaccine; immune system disorder; haematopoietic cell disorder;
KW   cancer; autoimmune disorder; rheumatoid arthritis; glomerulonephritis;
KW   HIV infection; anaemia; thrombocytopenia blood coagulation disorder;
KW   blood platelet disorder; wound; heart attack; myocardial infarction;
KW   stroke; scarring; asthma; graft-versus host rejection; inflammation;
KW   hyperproliferative disorder; lymphoproliferative disorder; arrhythmia;
KW   aberrant cellular division; cell proliferative disorder; angiogenesis;
KW   cardiovascular disorder; pulmonary heart disease; neovascularisation;
KW   hypertrophic scar; keloid; ocular disorder; diabetic retinopathy;
KW   uveitis; epithelial cell proliferation; neurological disease; apoptosis;
KW   Parkinson's disease; Alzheimer's disease; Huntington's chorea; ALS; AIDS;
KW   amyotrophic lateral sclerosis; toxin induced liver disease; septic shock;
KW   cachexia; anorexia; lung damage; infection.
XX
OS   Homo sapiens.
XX
PN   US2003065151-A1.
XX
PD   03-APR-2003.
XX
PF   04-APR-2002; 2002US-00115123.
XX
PR   16-JUN-1998;   98US-0089507P.
PR   16-JUN-1998;   98US-0089508P.
PR   16-JUN-1998;   98US-0089509P.
PR   16-JUN-1998;   98US-0089510P.
PR   22-JUN-1998;   98US-0090112P.
PR   22-JUN-1998;   98US-0090113P.
PR   15-JUN-1999;   99WO-US013418.
PR   14-DEC-1999;   99US-00461325.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Ni J, Rosen CA, Wei Y, Young P, Florence K, Soppet DR;
PI   Brewer LA, Endress GA, Carter KC, Mucenski M, Ebner R, Lafleur DW;
PI   Olsen H, Shi Y, Moore PA, Komatsoulis G;
XX
DR   WPI; 2003-531736/50.
DR   N-PSDB; ACH66650.
XX
PT   Novel antibody that binds specifically to a HCEJQ69 protein, useful for
PT   detecting the presence of a protein in a biological sample, and for
PT   treating cancers, autoimmune disorders and HIV infection.
XX
PS   Disclosure; SEQ ID NO 134; 176pp; English.
XX
CC   The invention relates to an isolated antibody or its fragment that
CC   specifically binds to a protein. The antibody is useful for detecting a
CC   protein in a biological sample, by contacting the biological sample with
CC   the antibody or its fragment and detecting the protein in the biological
CC   sample. The antibody is useful for purifying, detecting and targeting the
CC   human secreted proteins, including both in vitro and in vivo diagnostic
CC   and therapeutic methods. The antibody is useful for immunophenotyping of
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CC   cell lines in biological samples and in antibody-based therapies for
CC   treating, inhibiting and preventing diseases, disorders or conditions
CC   associated with aberrant expression and/or activity of the above
CC   proteins. The antibody is useful for treating deficiencies or disorders
CC   of immune system and haematopoietic cells, for increasing differentiation
CC   and proliferation of haematopoietic cells, for treating immune
CC   deficiencies or disorders e.g. cancers, autoimmune disorders (such as
CC   rheumatoid arthritis and glomerulonephritis), HIV infection, anaemia and
CC   thrombocytopenia and as a marker for a particular immune system disease
CC   or disorder. The antibody is also useful for treating blood coagulation
CC   disorders, blood platelet disorders, wounds, heart attacks (infarction),
CC   strokes, scarring and asthma. The antibody is also useful for treating or
CC   preventing graft-versus host rejection, for modulating inflammation, for
CC   treating hyperproliferative disorders e.g. lymphoproliferative disorders
CC   and cancers, for inhibiting aberrant cellular division and for treating
CC   cell proliferative disorders. The antibody is also useful for treating
CC   cardiovascular disorders e.g. pulmonary heart disease and arrhythmia,
CC   disorders associated with neovascularisation and angiogenesis, for
CC   treating hypertrophic scars and keloids, ocular disorders e.g. diabetic
CC   retinopathy and uveitis, for wound healing and disorders of epithelial
CC   cell proliferation. The antibody is also useful for treating neurological
CC   diseases e.g. Parkinson's disease, Alzheimer's disease, Huntington's
CC   chorea and amyotrophic lateral sclerosis (ALS), diseases associated with
CC   increased apoptosis e.g. AIDS, toxin induced liver disease, septic shock,
CC   cachexia and anorexia, for preventing and healing damage to lungs and for
CC   treating infectious diseases. The present sequence represents the amino
CC   acid sequence of a novel human secreted protein. Note: the sequence data
CC   for this patent did not form part of the printed specification but was
CC   obtained in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20030065151
XX
SQ   Sequence 415 AA;

  Query Match             100.0%;  Score 395;  DB 6;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  395;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 79

Qy         61 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 139

Qy        121 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 199

Qy        181 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 259

Qy        241 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 319

Qy        301 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 379

Qy        361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 395
              |||||||||||||||||||||||||||||||||||
Db        380 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 8
AAM78898
ID   AAM78898 standard; protein; 414 AA.
XX
AC   AAM78898;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human protein SEQ ID NO 1560.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US004098.
XX
PR   03-FEB-2000; 2000US-00496914.
PR   27-APR-2000; 2000US-00560875.
PR   20-JUN-2000; 2000US-00598075.
PR   19-JUL-2000; 2000US-00620325.
PR   01-SEP-2000; 2000US-00654936.
PR   15-SEP-2000; 2000US-00663561.
PR   20-OCT-2000; 2000US-00693325.
PR   30-NOV-2000; 2000US-00728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y;
PI   Ma Y,  Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   N-PSDB; AAK52031.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT   in diagnosis and gene therapy.
XX
PS   Claim 20; Page 3878-3879; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC   (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC   sequence listing were missing at the time of publication
XX
SQ   Sequence 414 AA;

  Query Match             84.6%;  Score 334;  DB 4;  Length 414;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  334;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 79

Qy         61 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 139

Qy        121 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 199

Qy        181 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        200 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 259

Qy        241 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 319

Qy        301 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 334
              ||||||||||||||||||||||||||||||||||
Db        320 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 353


RESULT 9
AAU05759
ID   AAU05759 standard; protein; 358 AA.
XX
AC   AAU05759;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human NOV7 polypeptide #2.
XX
KW   Human; NOV7; AL132990 B; fertility disorder; spermatogenesis; cardiant;
KW   cytostatic; immunomodulatory; antiproliferative; antidiabetic;
KW   cell proliferation; cancer; diabetic retinopathy; angiogenic disorder;
KW   pulmonary disorder; haematopoietic disorder; immunological disorder;
KW   inflammatory disorder; tumour related disorders; emphysema; cirrhosis;
KW   wound healing; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 311. .322
FT                   /label= OTHER
FT                   /note= "Other= Unknown"
XX
PN   WO200149729-A2.
XX
PD   12-JUL-2001.
XX
PF   05-JAN-2001; 2001WO-US000299.
XX
PR   06-JAN-2000; 2000US-0174724P.
PR   11-JAN-2000; 2000US-0175434P.
PR   11-JAN-2000; 2000US-0175488P.
PR   12-JAN-2000; 2000US-0175696P.
PR   12-JAN-2000; 2000US-0175743P.
PR   13-JAN-2000; 2000US-0175819P.
PR   07-AUG-2000; 2000US-0223524P.
PR   04-JAN-2001; 2001US-00755665.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Prayaga SK,  Majumder K,  Taillon BE,  Spaderna SK,  Spytek KA;
PI   Macdougall J;
XX
DR   WPI; 2001-418356/44.
XX
PT   Nucleic acids encoding polypeptides, designated NOVX polypeptides, useful
PT   for treating a syndrome associated with a NOVX-associated disorder, e.g.
PT   cell proliferation (e.g. cancer and diabetic retinopathy), angiogenic or
PT   pulmonary disorder.
XX
PS   Disclosure; Page 33; 144pp; English.
XX
CC   The invention relates to nucleic acids encoding NOVX (X being an integer
CC   from 1-8) polypeptides. The NOVX nucleic acids and polypeptides are
CC   useful in diagnosing, treating or manufacturing a medicament for a
CC   disease or disorder associated with NOVX e.g. cell proliferation (cancer
CC   and diabetic retinopathy), angiogenic or pulmonary disorders, fertility
CC   disorders (e.g of spermatogenesis), haematopoietic, immunological,
CC   inflammatory and tumour related disorders, emphysema, cirrhosis, wound
CC   healing. NOVX nucleic acids are also useful in gene therapy. They are
CC   also used for screening for a modulator of activity or of latency or
CC   predisposition to a NOVX-associated disorder. They are also useful for
CC   determining the presence of or predisposition to a NOVX-associated
CC   disorder. The present sequence represents a version of NOV7 (AL132990 B)
CC   appearing in table 25 of the specification, which has sequence homology
CC   to an unidentified human secreted protein (HWHGUS54) and to alpha1 anti-
CC   trypsin
XX
SQ   Sequence 358 AA;

  Query Match            78.5%;  Score 310;  DB 4;  Length 358;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-299;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLH 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLH 60

Qy         95 EGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMA 154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMA 120

Qy        155 QKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKN 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKN 180

Qy        215 SSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFS 274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFS 240

Qy        275 RWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 334
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 RWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 300

Qy        335 HKAELKMDER 344
              ||||||||||
Db        301 HKAELKMDER 310


RESULT 10
ABB11832
ID   ABB11832 standard; peptide; 431 AA.
XX
AC   ABB11832;
XX
DT   11-JAN-2002  (first entry)
XX
DE   Human secreted protein homologue, SEQ ID NO:2202.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW   haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW   inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW   proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW   myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW   chronic inflammatory condition; proliferative retinopathy;
KW   atherosclerosis; coronary heart disease; arterial ischaemia;
KW   bone disorder; osteoporosis; vascular growth disorder;
KW   tissue regeneration; wound healing; infection; immune disorder;
KW   cell culture; drug screening; gene therapy; antiinflammatory;
KW   antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW   cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW   antifungal; vulnerary; antiulcer.
XX
OS   Homo sapiens.
XX
PN   WO200157188-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US003800.
XX
PR   03-FEB-2000; 2000US-00496914.
PR   27-APR-2000; 2000US-00560875.
XX
```

```
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-457740/49.
DR   N-PSDB; ABA09076.
XX
PT   Human proteins and DNA encoding sequences useful for preventing, treating
PT   or ameliorating a medical condition in a mammalian subject e.g. arthritis
PT   and cancer.
XX
PS   Claim 20; Page 263; 1963pp; English.
XX
CC   Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC   sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC   invention also relates to vectors and recombinant host cells comprising a
CC   nucleotide of the invention, methods of producing the novel polypeptides,
CC   antibodies against the polypeptides, methods of detecting the nucleotides
CC   or polypeptides in a sample, and methods of identifying compounds which
CC   bind to polypeptides of the invention. Although novel, many of the
CC   polypeptides of the invention have homology to known proteins, thereby
CC   giving an insight into their probable biological activities, and hence
CC   potential therapeutic applications. The polypeptides of the invention may
CC   have various activities, including cytokine, cell proliferation or cell
CC   differentiation activities; stem cell growth factor activity;
CC   haematopoiesis regulatory activity; tissue growth activity;
CC   immunomodulatory activity; activin- or inhibin-related activities;
CC   chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC   thrombolytic activities; receptor or ligand activities; or may be
CC   involved in oncogenesis, cancer cell proliferation or metastasis.
CC   Depending on their biological activities, polypeptides and nucleotides of
CC   the invention are useful for preventing, treating or ameliorating medical
CC   conditions, e.g., by protein or gene therapy. Such conditions include
CC   cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC   disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC   proliferative retinopathy, atherosclerosis, coronary heart disease,
CC   arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC   vascular growth. Polypeptides involved with tissue regeneration and
CC   repair (or nucleic acids encoding them) may be used to promote wound
CC   healing (e.g., of burns, incisions and ulcers), while those with
CC   immunomodulatory activities may be used in the treatment of viral,
CC   bacterial and fungal infections in addition to immune disorders.
CC   Polypeptides with growth factor activity may be used in cell cultures to
CC   promote cell growth. For example, such polypeptides may be used to
CC   manipulate stem cells in culture to give rise to neuroepithelial cells
CC   that can be used to augment or replace cells damaged by illness,
CC   autoimmune disease or accidental damage. The polypeptides and nucleotides
CC   may also be used in the diagnosis of the above conditions, and in drug
CC   screening techniques. The present sequence represents a novel human
CC   polypeptide of the invention
XX
SQ   Sequence 431 AA;

  Query Match             43.0%;  Score 170;  DB 4;  Length 431;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-160;
  Matches  170;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        165 KTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFR 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 KTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFR 260

Qy        225 SGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRV 284
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 SGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRV 320

Qy        285 VDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 334
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 VDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 370


RESULT 11
AAM79882
ID   AAM79882 standard; protein; 431 AA.
XX
AC   AAM79882;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human protein SEQ ID NO 3528.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US004098.
XX
PR   03-FEB-2000; 2000US-00496914.
PR   27-APR-2000; 2000US-00560875.
PR   20-JUN-2000; 2000US-00598075.
PR   19-JUL-2000; 2000US-00620325.
PR   01-SEP-2000; 2000US-00654936.
PR   15-SEP-2000; 2000US-00663561.
PR   20-OCT-2000; 2000US-00693325.
PR   30-NOV-2000; 2000US-00728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y;
PI   Ma Y,  Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   N-PSDB; AAK53015.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT   in diagnosis and gene therapy.
XX
PS   Claim 20; Page 371; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC   (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC   sequence listing were missing at the time of publication
XX
SQ   Sequence 431 AA;

  Query Match             43.0%;  Score 170;  DB 4;  Length 431;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-160;
  Matches  170;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        165 KTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFR 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 KTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFR 260

Qy        225 SGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRV 284
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 SGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRV 320

Qy        285 VDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 334
              ||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        321 VDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 370

RESULT 12
AAM70426
ID   AAM70426 standard; protein; 140 AA.
XX
AC   AAM70426;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human bone marrow expressed probe encoded protein SEQ ID NO: 30732.
XX
KW   Human; bone marrow expressed exon; gene expression analysis; probe;
KW   microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS   Homo sapiens.
XX
PN   WO200157276-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000668.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488900/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for analyzing
PT   gene expression in human bone marrow.
XX
PS   Example 4; SEQ ID NO 30732; 658pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   bone marrow. They can be used to measure gene expression in bone marrow
CC   samples, which may enable the improved diagnosis and treatment of cancers
CC   such as lymphoma, leukaemia and myeloma. The present sequence is a
CC   protein encoded by one of the probes of the invention
XX
SQ   Sequence 140 AA;

  Query Match             32.7%;  Score 129;  DB 4;  Length 140;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-119;
  Matches  129;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         64 FSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLFIDQ 123
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 FSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLFIDQ 60

Qy        124 RLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPGTVM 183
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPGTVM 120

Qy        184 LLANYIFFR 192
              |||||||||
Db        121 LLANYIFFR 129


Search completed: March 31, 2006, 10:02:30
Job time : 212.427 secs
```

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 10:02:58 ; Search time 24.9011 Seconds
(without alignments)
1526.262 Million cell updates/sec

Title: US-10-664-356-1562_COPY_20_414
Perfect score: 395
Sequence: 1 LLKPSFSPRNYKALSEVQGW.....YSEKIPSVLFLGKIVNPIGK 395

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word_size : 15

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description

No matches found

Search completed: March 31, 2006, 10:08:39
Job time : 24.9011 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 09:55:21 ; Search time 149.895 Seconds
(without alignments)
1859.193 Million cell updates/sec

Title: US-10-664-356-1562_COPY_20_414
Perfect score: 395
Sequence: 1 LLKPSFSPRNYKALSEVQGW.....YSEKIPSVLFLGKIVNPIGK 395

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size: 15

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	395	100.0	414	2	Q8IW75_HUMAN	Q8iw75 homo sapien
2	19	4.8	413	2	Q7TMF5_MOUSE	Q7tmf5 mus musculu
3	19	4.8	413	2	Q9CQ32_MOUSE	Q9cq32 m mus muscu
4	19	4.8	413	2	Q6P6M3_MOUSE	Q6p6m3 mus musculu
5	16	4.1	411	2	Q8R4Z1_RAT	Q8r4z1 rattus norv

ALIGNMENTS

RESULT 1
Q8IW75_HUMAN
ID Q8IW75_HUMAN PRELIMINARY; PRT; 414 AA.
AC Q8IW75;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Serine (Or cysteine) proteinase inhibitor, clade A (Alpha-1
DE antiproteinase, antitrypsin), member 12 (OL-64) (Visceral adipose-
DE specific SERPIN).
GN Name=SERPINA12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RG NIH MGC Project;
RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RA Chen S., Guo J.H., Yu L.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Hida K., Wada J., Zhang H.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Belongs to the serpin family.
DR EMBL; BC040857; AAH40857.1; -; mRNA.
DR EMBL; AY177692; AAO18649.1; -; mRNA.
DR EMBL; AY326420; AAP88384.1; -; mRNA.
DR HSSP; P01009; 1QMB.
DR Ensembl; ENSG00000165953; Homo sapiens.
DR HGNC; HGNC:18359; SERPINA12.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
KW Serpin.
SQ SEQUENCE 414 AA; 47175 MW; 5C70F1AB5935661C CRC64;

Query Match 100.0%; Score 395; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 79

Qy         61 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 139

Qy        121 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 199

Qy        181 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 259

Qy        241 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 319

Qy        301 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        320 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 379

Qy        361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 395
              |||||||||||||||||||||||||||||||||||
Db        380 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 2
Q7TMF5_MOUSE
ID   Q7TMF5_MOUSE PRELIMINARY;      PRT;   413 AA.
AC   Q7TMF5;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Visceral adipose-specific SERPIN.
GN   Name=Serpina12;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Swiss Webster;
RA   Hida K., Wada J., Zhang H.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the serpin family.
DR   EMBL; AY326419; AAP88383.1; -; mRNA.
DR   HSSP; P01008; 1ATH.
DR   MGI; MGI:1915304; Serpina12.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR000295; Prot_inh_Lserp2.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   Pfam; PF00079; Serpin; 1.
DR   PRINTS; PR00780; LEUSERPINII.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Serpin.
SQ   SEQUENCE   413 AA;  47674 MW;  EE2B3B08C2DD418F CRC64;

  Query Match             4.8%;  Score 19;  DB 2;  Length 413;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-10;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        325 HRSLKVGEAVHKAELKMDE 343
              |||||||||||||||||||
Db        344 HRSLKVGEAVHKAELKMDE 362


RESULT 3
Q9CQ32_MOUSE
ID   Q9CQ32_MOUSE PRELIMINARY;      PRT;   413 AA.
AC   Q9CQ32;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched
DE   library, clone:4632419J12 product:hypothetical Serpins containing
DE   protein, full insert sequence (Mus musculus 17 days embryo head cDNA,
DE   RIKEN full-length enriched library, clone:3300001F13
DE   product:hypothetical Serpins containing protein, full insert
DE   sequence).
GN   Name=Serpina12;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
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RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the serpin family.
DR   EMBL; AK014589; BAB29447.1; -; mRNA.
DR   EMBL; AK014346; BAB29287.1; -; mRNA.
DR   HSSP; P01008; 1ATH.
DR   Ensembl; ENSMUSG00000041567; Mus musculus.
DR   MGI; MGI:1915304; Serpina12.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR000295; Prot_inh_Lserp2.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   Pfam; PF00079; Serpin; 1.
DR   PRINTS; PR00780; LEUSERPINII.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Hypothetical protein; Serpin.
SQ   SEQUENCE   413 AA;  47634 MW;  D0AE8E1EE24FD60A CRC64;

  Query Match             4.8%;  Score 19;  DB 2;  Length 413;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-10;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        325 HRSLKVGEAVHKAELKMDE 343
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Db        344 HRSLKVGEAVHKAELKMDE 362


RESULT 4
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ID   Q6P6M3_MOUSE PRELIMINARY;      PRT;   413 AA.
AC   Q6P6M3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Visceral adipose-specific SERPIN.
GN   Name=Serpina12;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Jaw and Limb;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Jaw and Limb;
RG   NIH MGC Project;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the serpin family.
DR   EMBL; BC062143; AAH62143.1; -; mRNA.
DR   HSSP; P01008; 1ATH.
DR   Ensembl; ENSMUSG00000041567; Mus musculus.
DR   MGI; MGI:1915304; Serpina12.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR000295; Prot_inh_Lserp2.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   Pfam; PF00079; Serpin; 1.
DR   PRINTS; PR00780; LEUSERPINII.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW   Serpin.
SQ   SEQUENCE   413 AA;  47630 MW;  CE1940BA2EE35811 CRC64;

  Query Match             4.8%;  Score 19;  DB 2;  Length 413;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-10;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        325 HRSLKVGEAVHKAELKMDE 343
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Db        344 HRSLKVGEAVHKAELKMDE 362


RESULT 5
Q8R4Z1_RAT
ID   Q8R4Z1_RAT  PRELIMINARY;      PRT;   411 AA.
AC   Q8R4Z1;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Visceral adipose tissue specific SERPIN.
GN   Name=Serpina12; Synonyms=Vaspin;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=OLETF; TISSUE=Visceral adipose;
RA   Hida K., Wada J., Zhang H., Shikata K., Makino H.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the serpin family.
DR   EMBL; AF245398; AAL99574.1; -; mRNA.
DR   HSSP; P01008; 1ATH.
DR   Ensembl; ENSRNOG00000009710; Rattus norvegicus.
DR   RGD; 708485; Serpina12.
DR   GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR   InterPro; IPR000295; Prot_inh_Lserp2.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   Pfam; PF00079; Serpin; 1.
DR   PRINTS; PR00780; LEUSERPINII.
DR   SMART; SM00093; SERPIN; 1.
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KW   Serpin.
SQ   SEQUENCE   411 AA;  47527 MW;  29FA271FF8CC8A2D CRC64;

  Query Match             4.1%;  Score 16;  DB 2;  Length 411;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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GenCore version 5.1.7

OM protein - protein search, using sw model

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Gapop 60.0 , Gapext 60.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	395	100.0	414	2	US-09-755-665-14	Sequence 14, Appl
2	395	100.0	414	2	US-09-755-665-55	Sequence 55, Appl
3	395	100.0	414	2	US-09-755-665-56	Sequence 56, Appl
4	395	100.0	415	2	US-09-461-325-134	Sequence 134, App
5	395	100.0	415	2	US-10-012-542-134	Sequence 134, App
6	395	100.0	415	2	US-10-115-123-134	Sequence 134, App
7	310	78.5	361	2	US-09-755-665-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1
US-09-755-665-14
; Sequence 14, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Taillon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-14

Query Match 100.0%; Score 395; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 120
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Qy        301 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 360
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Db        320 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 379

Qy        361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 395
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Db        380 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
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RESULT 2
US-09-755-665-55
; Sequence 55, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Taillon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-55

Query Match 100.0%; Score 395; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 60
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 79

Qy         61 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 139

Qy        121 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 199

Qy        181 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 259

Qy        241 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 319

Qy        301 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 379

Qy        361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 395
                 |||||||||||||||||||||||||||||||||||
Db        380 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
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RESULT 3
US-09-755-665-56
; Sequence 56, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Taillon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-56

Query Match 100.0%; Score 395; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 79

Qy         61 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 139

Qy        121 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 199

Qy        181 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 259

Qy        241 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 319

Qy        301 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 379

Qy        361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 395
                 |||||||||||||||||||||||||||||||||||
Db        380 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
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RESULT 4
US-09-461-325-134
; Sequence 134, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: PZ029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (415)
; OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring L-amino acids
US-09-461-325-134

Query Match 100.0%; Score 395; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 79

Qy         61 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 139

Qy        121 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 199

Qy        181 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 259

Qy        241 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 319
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Qy        301 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 379

Qy        361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 395
              |||||||||||||||||||||||||||||||||||
Db        380 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 5
US-10-012-542-134
; Sequence 134, Application US/10012542
; Patent No. 6627741
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029P1
;  CURRENT APPLICATION NUMBER: US/10/012,542
;  CURRENT FILING DATE:  2001-12-12
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
;   LENGTH: 415
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (415)
;   OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring L-amino
;   OTHER INFORMATION: acids
US-10-012-542-134

  Query Match            100.0%;  Score 395;  DB 2;  Length 415;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  395;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 79

Qy         61 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 139

Qy        121 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 199

Qy        181 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 259

Qy        241 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 319

Qy        301 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 379

Qy        361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 395
              |||||||||||||||||||||||||||||||||||
Db        380 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414


RESULT 6
US-10-115-123-134
; Sequence 134, Application US/10115123
; Patent No. 6774216
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029G30AP1D2
;  CURRENT APPLICATION NUMBER: US/10/115,123
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: PCT/US99/13418
;  PRIOR FILING DATE: 1999-06-15
;  PRIOR APPLICATION NUMBER: 60/089,507
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,508
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,509
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,510
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/090,112
;  PRIOR FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: 60/090,113
;  PRIOR FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
;   LENGTH: 415
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (415)
;   OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring L-amino acids
US-10-115-123-134

  Query Match            100.0%;  Score 395;  DB 2;  Length 415;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  395;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 LLKPSFSPRNYKALSEVQGWKQRMAAKELARQNMDLGFKLLKKLAFYNPGRNIFLSPLSI 79

Qy         61 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 STAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLF 139

Qy        121 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMAQKQINDFISQKTHGKINNLIENIDPG 199

Qy        181 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 TVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKNSSVKVPMMFRSGIYQVGYDDKLSCTI 259

Qy        241 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFSRWKTLLSRRVVDVSVPRLHMTGTFDL 319

Qy        301 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 KKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAVHKAELKMDERGTEGAAGTGAQTLPME 379

Qy        361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 395
              |||||||||||||||||||||||||||||||||||
Db        380 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
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RESULT 7
US-09-755-665-57
; Sequence 57, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
;  APPLICANT: Prayaga, Sudhirdas K.
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Taillon, Bruce E.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  MacDougall, John
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-631
;  CURRENT APPLICATION NUMBER: US/09/755,665
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
;   LENGTH: 361
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)..(361)
;   OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
;   OTHER INFORMATION: specification
US-09-755-665-57

  Query Match            78.5%;  Score 310;  DB 2;  Length 361;
  Best Local Similarity  100.0%;  Pred. No. 8.1e-294;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLH 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DLGFKLLKKLAFYNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNFRKMPEKDLH 60

Qy         95 EGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMA 154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EGFHYIIHELTQKTQDLKLSIGNTLFIDQRLQPQRKFLEDAKNFYSAETILTNFQNLEMA 120

Qy        155 QKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKN 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QKQINDFISQKTHGKINNLIENIDPGTVMLLANYIFFRARWKHEFDPNVTKEEDFFLEKN 180

Qy        215 SSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFS 274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSVKVPMMFRSGIYQVGYDDKLSCTILEIPYQKNITAIFILPDEGKLKHLEKGLQVDTFS 240

Qy        275 RWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 334
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 RWKTLLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTKIAPHRSLKVGEAV 300

Qy        335 HKAELKMDER 344
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Db        301 HKAELKMDER 310


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Job time : 33.225 secs
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